166082, 2, Appli 1223, Ap 148813,

Sequence Sequence Sequence 9, Appli 9, Appli 9, Appli 102913,

Sequence 2, Appli Sequence 1223, Appli Sequence 12266, Sequence 115627, Sequence 125194, Sequence 151194, Sequence 123119, Sequence 123119, Sequence 123119, Sequence 123119, Sequence 123119, Sequence 13306, Sequence 13619, Sequence 192786, Sequence 19619, Sequence 109918, Sequence 109994, Sequence 109994, Sequence 109994, Sequence 16619, Sequence 16619,

Scoring table:

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Sequence 63986,

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Publication No. US20040146884A1

FUNDERREAL INFORMATION:

APPLICANT: Benmer, Jercen

APPLICANT: Benk, Michael Andrew

APPLICANT: Benk, Michael Andrew

APPLICANT: Benk, Michael Andrew

APPLICANT: Bish, Steven A

TITLE OF INVENTION: Antifreeze proteins isolated from forage

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TITLE OF INVENTION: Antifreeze proteins isolated

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1385
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US-10-657-852-20
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US-10-657-852-19
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Maximum DB seq length: 2000000000
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                                                      121 RLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVS
61 CCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQI
                                    RLKSLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVS
                                                                                                                                                                                                                                                                                        Sequence 17, Application US/10657852

Subjication No. US20040146884A1

GENERAL INFORMATION:

APPLICANT: Demmer, Jeroen

APPLICANT: Ball, Claire

APPLICANT: Hall, Claire

APPLICANT: Fish, Steven A

TITLE OF INVENTION: Grasses and methods for their use.

TITLE OF INVENTION: ALLIÉTEZE PROTEINS isolated from forage

TITLE OF INVENTION: Grasses and methods for their use.

TITLE OF INVENTION: Grasses and methods for their use.

CURRENT FILING DATE: 2003-09-09

RICHARDA PELICATION NUMBER: 60/409,557

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17

TYPE: PRT
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OTHER INFORMATION: Xaa = Any Amino Acid
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Best Local Similarity
Matches 251; Conserv
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US-10-657-852-17
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US-10-657-852-24
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Sequence 24, Application US/10657852; Publication No. US20040146884A1; GENERAL INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                       Length 262;
APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire
APPLICANT: Hall, Claire
APPLICANT: Fish, Steven A
TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: grasses and methods for their use.
FILE REPERBENCE: 11000.10700
CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT APPLICATION NUMBER: 60/409,557
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.8%; Score 980.5; DB 18; Length Best Local Similarity 73.5%; Pred. No. 1.7e-76; Matches 194; Conservative 24; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                           39; Indels
                                                                                                                                                                                                                                                                                                                                                         DB 18;
                                                                                                                                                                                                                                                                                                                                                       71.7%; Score 992.5; DB 175.0%; Pred. No. 1.6e-77; ive 22; Mismatches 39
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PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
LENGTH: 254
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ORGANISM: Festuca arundinacea
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Matches 198; Conservative
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110 LVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSN 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 NAVSGNDNTVMCGNNNTVSGSNNTISSGSDNIVTGSNHIVCGTKHIITDNNNDVSGNDNN 237
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                                APPLICANT: Demmer, Jeroen
APPLICANT: Shenk, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Steven A
TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: Grasses and methods for their use.
TITLE OF INVENTION: JUNOU 1070U
CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT FILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE FASTSEQ for Windows Version 4.0
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Best Local Similarity 67.5%; Pred. No. 2.1e-70;
Matches 187; Conservative 20; Mismatches 51.
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US-10-657-852-19
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LENGTH: 277
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LENGTH: 277
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                                                                                WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
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61
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; Publication No. US20040146884A1
; GRERAL INFORMATION:
APPLICANT: Bemmer, Jercen
; APPLICANT: Bhenk, Michael Andrew
; APPLICANT: Bhenk, Michael Andrew
; APPLICANT: Brish, Steven A
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
; TITLE OF INVENTION: Areases and methods for their use.;
FILE REFERENCE: 11000.1070U
; CURRENT APPLICATION NUMBER: US/10/657,852
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; RIUNG DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 25
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US-10-657-852-20
; Sequence 20, Application US/10657852
; Publication No. US20040146884A1
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Gaps

19;

51; Indels

Length 277;

DB 18;

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19;
Sequence 19, Application US/10657852

Publication No. US20040146884A1

GENERAL INFORMATION:

APPLICANT: Demarr. Jercen

APPLICANT: Shenk, Michael Andrew

APPLICANT: Fish, Michael Andrew

TITLE OF INVENTION: Antifreeze proteins isolated from forage

TITLE OF INVENTION: Antifreeze proteins isolated from forage

TITLE OF INVENTION: Grasses and methods for their use.

FILE REFERENCE: 11000.1070U

CURRENT APPLICATION NUMBER: US/10/657,852

CURRENT FILING DATE: 2003-09-09

PRIOR FILING DATE: 2002-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 65.6%; Score 908.5; DB 18; Length 277; Best Local Similarity 67.9%; Pred. No. 3.1e-70; Matches 188; Conservative 19; Mismatches 51; Indels 19;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20040146884A1
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Matches 186; Conservative
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LENGTH: 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 EGVGCETASGRVVALRLP-------KRGLGGIIPSSIGELDHLRYLDLSGNS 109
                                                                                                                                                                                       169 NVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNN 228
                                                                                                                                                                                                                                                                        178 NAVSGNDNTVICGNNNTVSGSNNTIVSGSDNIVTGSNQVVCGTKHIITDNNNDVSGNDNN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 EGVGCDGTSGRVTALRLPISLEDCGKLKSLNLANERLVGTIPSWIGELDHHCYLVLSDNS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 LVGEVP----KSLQIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG 224
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    MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                           1 MAKCWILLIFIVVLLPPASAT--SCHPDDLRALRGFVGNLNG-GGVLLHGAWSGSLCCAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 26, Application US/10657852
Publication No. US20040146884A1
GENERAL INFORMATION:
APPLICANT: Demmer, Jeroen
APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire
APPLICANT: Fish, Steven A
TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: grasses and methods for their use.
FILE REFERENCE: 11000.1070U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.3%; Score 904.5; DB 18; Length Best Local Similarity 66.5%; Pred. No. 7.1e-70; Matches 187; Conservative 20; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NDNNVSGSFHTVSGEHNTVSGSNNTVSGSNH1VSGSNKVVT 265
                                                                                                                                                                                                                                                                                                                                 229 VSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265
                                                                                                                                                                                                                                                                                                                                                  238 VSGSSHTVSGSHNTVSGSNNTVSGSNHVVSGSNKVVT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT FILING DATE: 2003-09-09
PRIOR PILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PASLSEQ for Windows Version 4.0
EEQ ID NO 26
LENGTH: 281
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US-10-657-852-18
; Sequence 18, Application US/10657852
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ORGANISM: Lolium perenne
US-10-657-852-26
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109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS
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Sequence 22, Application US/10657852;
Publication No. US20040146884A1
GENERAL INFORMATION:
APPLICANT: Demmer, Jercen
APPLICANT: Hall, Claire
APPLICANT: Finenk, Michael Andrew
APPLICANT: Fish, Steven
TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: QUARRER: 11000.1070U
CURRENT APPLICATION NUMBER: 05/10/657,852
CURRENT FILING DATE: 2003-09-09
FRIOR PILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 65.1%; Score 901.5; DB 18; Length 285; Best Local Similarity 65.5%; Pred. No. 1.3e-69; Matches 186; Conservative 17; Mismatches 54; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 281;
GENERAL INFORMATION:
APPLICANT: Demmer, Jeroen
APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire
APPLICANT: Hill, Claire
APPLICANT: Fish, Steven A
ITILE OF INVENTION: Antifreeze proteins isolated from forage
ITILE OF INVENTION: ANTIFREE 2003-109-09
CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT APPLICATION NUMBER: 60/409,557
PRIOR FILING DATE: 2002-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.1%; Score 901.5; DB 18; Length 66.2%; Pred. No. 1.3e-69; ive 21; Mismatches 51; Indels
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65 EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124
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Sequence 19, Application US/108-7832,
Sequence 19, Application US/108-7832,
GENERAL INFORMATION:
APPLICANT: Demen: Jeroen
APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire
APPLICANT: Hall, Claire
APPLICANT: Hall, Claire
APPLICANT: Hall, Claire
TITLE OF INVENTION: Grasses and methods for their use.
TITLE OF INVENTION: Grasses and methods for their use.
FILE REPRENCE: 11000-1070U
CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT FILING DATE: 2003-09-09
PRIOR PELLOR DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.2%; Score 668; DB 18; 53.0%; Pred. No. 1.7e-49;
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Matches 151; Conservative 17; Mismatches
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                                                                                                                    -----GIIPSSIGELDHLRYLD 104
                                                                                                                                                                 62 NGASGRITTLWLPRRGLAGTITGASLAGLARLESLNLANNRLVGTIPSWIGELDHLLYLD 121
                                                                                                                                                                                                                          LSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGTNNSV 163
                                                                                                                                                                                                                                                    164 GSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS 223
                                                                                                                                                                                                                                                                                                                                                                   182 LSGRNNVVSGNDNTVISENNNTVSGSFNTVITGSDNVLTGSNHVVSGRSHIVTDNNNSVS 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 ETASGRVVALRLPKRGLG---------GIPSSIGELDHLRYLD 104
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                                    3 LILIFIAFILPVACAATSSCHPDDLRALRGFAKNLGG-GGVLLRTAWSGTSCCVWEGVGC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 GNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/10657852

Publication No. US20040146884A1

GENERAL INFORMATION:
APPLICANT: Demmer. Jeroen
APPLICANT: Demmer. Jeroen
APPLICANT: Shewk, Michael Andrew
APPLICANT: Fish, Steven A
TITLE OF INVENTION: Artifreeze proteins isolated from forage
TITLE OF INVENTION: QUARRER OF 11000.1070U
CURRENT FILING DATE: 2003-09-09

PRIOR PRIOR FILING DATE: 2003-09-09

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 63.8%; Score 884; DB 18;
Best Local Similarity 65.5%; Pred. No. 4.2e-68;
Matches 186; Conservative 14; Mismatches 52;
                                                                                                                 ETASGRVVALRLPKRGLG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Festuca arundinacea
US-10-657-852-21
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US-10-657-852-15
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Gaps

64;

Length 243;

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LTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNN 183
                                                                                                                                                                                                           139 NVVSGSHNTVVFGGDNFLSGSNHVVSGNHHVVTDNKNAVSGDHNTVSGSQNTVSGNHHII 198
APPLICANT: Demmer, Jeroen
APPLICANT: Demmer, Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire
APPLICANT: Hall, Claire
APPLICANT: Hish, Steven A
TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: Grasses and methods for their use.
FILE REFERENCE: 11000.1070 us/10/657,852
CURRENT FILING DATE: 2003-09-09
CURRENT FILING DATE: 2003-09-09
NUMBER OF SEQ ID NOS: 44
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 243;
                                                                                                                                                                                                                                                              241 ------NTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                     199 SASHSTISGNHNTVSGSNNFVSGNNNIVSGSNHVVYGNNKVVTGG 243
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Pred. No. 2.2e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/10657852; Publication No. US20040146884A1; GENERAL INFORMATION:
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Best Local Similarity
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US-10-437-963-166082
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            APPLICANT:
APPLICANT:
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US-10-437-963-180288

i Sequence 180288, Application US/10437963

j Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: APPLICANT: Zhou, Yihua

APPLICANT: Boukharov, Andrey A.

APPLICANT: Buckharov, Andrey A.

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFREENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 180288

LEASTH: 1010

LEASTH: 1010
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                                                                                              65 EGYGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124
                                                                                                                                                                                          65 EGVGCETASGRVVALRIPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124
                                                                                                                                                                      125 LTTDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNN 183
                                                                                                                                                                                                                                        184 NHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTV 243
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                                                                                                                                58 kGVGCDGASGCV-----KSFQILLKG 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 KCCML-LVFLGFILQVAGATSWSCHHDDLHALRGLAENLS-GKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 DGVACD-AAARVTALRLPGRGLEGPIPPSLAALARLQDLDLSHNALT-------
                                5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                  1 MAKCWOLLIFLALLIPAASAA - - SCHPDDLYALRDFAGNIRG - GGVLLRAALPGASCCGW
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Gaps
64;
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18.9%; Score 262; DB 16; Length 1010;
Best Local Similarity 40.1%; Pred. No. 1.3e-13;
Matches 71; Conservative 19; Mismatches 53; Indels 34
                                                                                                                                                                                                                                                                                                                                -----NNTVSGSNHIVSGSNKVVTDG 267
55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_7766C.1.pep
US-10-437-963-180288
Mismatches
 18;
 148; Conservative
                                                                                                                                                                                                                                                                                                                244 SGS------
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 Matches
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Sequence 166082, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION: APPLICANT: La ROSA, Thomas J.

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APPLICANT: Wu, Wei APPLICANT: Wu, Wei APPLICANT: Boucharov, Andrey A. APPLICANT: Boucharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping Tric Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERBNCE: 38-21(5322) B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILLING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 166082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 CSWTGVSCSRQQPEKVIALQMNSCGLSGRISPFLGNLSFLKTLDLGNNQLVGQIPSELGH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 --QIRLKSLTTDSQSLGMGSIN------MLLHVSSRRTLDBEPNTI-SGTNNSVGSG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 LSKIRMINIST---NILRGSIPVEMRGCTKIMTLHIGNNQLQGEIPAEIGSSLKNLINLY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 -SNNVVSGN-----DNTVVSGNNNHVSGSNNTVVTGSDN--TVVGSNHVVSG---T 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 MAKCCMLLVFLGFILQV--AGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGAS-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CSWEGVGCETAS-GRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL--
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14.9%; Score 206.5; DB 16; Length 1039;
Best Local Similarity 29.1%; Pred. No. 8.6e-09;
Matches 83; Conservative 52; Mismatches 103; Indels 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KHIVTDNNNVVSGNDNNVSG-----SFHTVSGEHNTVSGS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Clone ID: PAT MRT4530_64826C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: October 8, 2005, 02:33:49 Job time : 166 secs
Χ.
Kovalic, David K
Zhou, Yihua
Cao, Yongwei
Wu, Wei
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ORGANISM: Oryza sativa
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Sequence 732, Application US/10101464A

Sequence 732, Application US/10101464A

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: LOGIC-2
CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT APPLICATION NUMBER: 09/704,302
PRIOR PAPLICATION NUMBER: 09/108,966
PRIOR FILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR PILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989

SEQ ID NO 732
LENGTHREE FREESE FREES FREESE FREES FREESE FREESE FREES FR
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                                                 214 IVTDNNNVVSGNDNNVSGSFHTVSGEHNTVS-----GSNNTVSGSNHIVSG---SN 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 CHHDDLHALRGLAENLSGKGAVRLRAAWS-GASCCSWEGVGCETASGR---VVALRLPKR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38 CNQSDVQALISFKQTVSSSSPLN----WEVNRSCCTWEGVTCGLLSLQQFSVTKLRLPGR 93
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Best Local Similarity 33.1%; Pred. No. 2.1e-08;
Matches 49; Conservative 24; Mismatches 60; Indels 15.
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Job time : 44 secs
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; ORGANISM: Pinus radiata
US-10-101-464A-732
                                                                                                                                                                          262 KVVT 265
                                                                                                                                                                                                                                                           224 KEAT 227
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US-10-101-464A-732
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104 NOAKGEHSTIAGGESNQATGRNSTVAGGSNNQAVGTNSTVAGGSNNQAKGANSFAAGVGN 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 NTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214 IVTDNNNVVSGNDNNVSGSFHTVSGEHNTVS-----GSNNTVSGSNHIVSG---SN 261
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Patent No. 6753417

GENERAL INFORMATION

GENERAL INFORMATION

APPLICANT: HANSEN, ERIC J.

APPLICANT: AEBI, CHRISTOPH

APPLICANT: AEBI, CHRISTOPH

APPLICANT: FREDENBURG, LESLIE D.

APPLICANT: FREDENBURG, ROSS A.

TITLE OF INVENTION USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS

FILE REFERENCE: AMCY:024

CURRENT FILING DATE: 1999-06-21

PRIOR APPLICATION NUMBER: US/09/952, 267B

CURRENT FILING DATE: 1999-06-21

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PATENTIN VET: 2.1

SEQ ID NO S: 98

SEQ ID NO S: 98

SEQ ID NO S: 98
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                                                                                                                                                                       APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
ITTLE OF INVENTION USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.3%; Score 170; DB 3; Length 624; 30.6%; Pred. No. 8.3e-08; ive 24; Mismatches 50; Indels 1
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                                            Sequence 7, Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: ABLI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Moraxella catarrhalis
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Best Local Similarity 30.65
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224 KEAT 227
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US-09-952-267B-7
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LENGTH: 624
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Fatent No. 6768041
GENERAL INFORMATION:
GENERAL INFORMATION:
FAPPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
FILE REFRENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2000-11-01
FRIOR APPLICATION NUMBER: 09/228,986
FRIOR FILING DATE: 1999-01-12
FRIOR FILING DATE: 1999-11-01
FRIOR FILING DATE: 1999-11-01
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
FRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SSOFTWARE: FastSEQ for Windows Version 4.0
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                                                    --- 188
                                                                                                                                                     ---SNNTVVTG-----SDNTVVGSNHVV---SGTKHIVTDNNNVVSGNDNN 228
                                                                                                                                                                                  61 QSWKGVSCSGSS--VTLIKLSGLGLSGSLYYQLSDLSSLTTLDLSNNNIQGNIPYALPQK 118
119 LQELNLASNGLS-GTIPYSISNMTGLTDLKLSHNQLSGQIQDIFGQLSSLSTLDLSFNTL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 LKSLTTDSQSLGMGSI-----NM------LLH-------VSSRTLDDEEPNTI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----NNSVGSGSNNVVSGNDNTVVSGNNNHVSG----- 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---SNNTVVTG-----SDNTVVGSNHVV---SGTKHIVTDNNNVVSGNDNN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 LQELNLASNGLS-GTIPYSISNMTGLTDLKLSHNQLSGQIQDIFGQLSSLSTLDLSFNTL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                 :
TQNLPQSFSSLSVLYLQNNQL-AGSVNVLANLPLTDLNIENNRFSGWVPNAWRSNQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 CMLLVFLGFILQVA---GATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 101; Gaps
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                                               -- NNSVGSGSNNVVSGNDNTVVSGNNNHVSG
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1 Similarity 26.1%; Pred. No. 8.9e-08;
81; Conservative 39; Mismatches 89
                                                                                                                                                                                                                                                                                                     287 KSLSGGAIVG 296
                                                                                                                                                                                                                                                      229 VSGSFHTVSG 238
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ORGANISM: Pinus radiata
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Best Local Similarity
Matches 81; Conserv
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                                               157 SGT---
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LENGTH: 707
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                                                                                                                                                                            Sequence 764, Application US/10101464A
; Sequence 764, Application US/10101464A
; Sequence 764, Application US/10101464A
; GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: and Their Use in the Modification of Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
; PRIOR FILING DATE: 2000-01-11
; WUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 764
; LENGTH: 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239 NCTSLTDLVISSNN-LSGP--IPSEFSGLVSLKFLFLDDNSISGSIPTSLVNCTSLFALK 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 TISG------TINISVGSGSINIVVSGNDITVVSGNN--NHVSGSNNTVV- 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --TGSDNTVVGSNHVVSGTKHIVTDNNNVVS-----GNDNNVSGSFHTVSGEHNT---VS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 SGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSGNSLVGEVPKSL----QIRLKSLTTDSQS-----LGMGSINMLLHVSSRRTLDEEPN 154
253 SRLVRLETLLFDDNSISGSIPASISNCTSLQYLDISDNSLSGP-----IPSEFSRL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 MLLVFLGFIL--------OVAGATSWSCHHD--DLHALRGLAE--NL
                                                                                304 VSLESLYFHDNSISGSIPTFLVNCTSLSALGASGNKLSGSIPSVMGLMKNIS 355
                                                        VS-----GNDNNVSGSFHTVSGEHNTVS----GSNNTVSGSNHIVSGSNKVVT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 323;
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Best Local Similarity 25.5
Matches 82; Conservative
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                                                                                                                                                        RESULT 9
US-10-101-464A-764
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Sequence 902, Application US/10101464A Patent No. 6768041
GENERAL INFORMATION: APPLICANT: Strabala, Timothy APPLICANT: Nieuwenhuizen, Nicolaas

US-10-101-464A-902

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APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
FRICH FILING DATE: 2000-11-01
FRICH PAPLICATION NUMBER: 09/704,302
FRICH APPLICATION NUMBER: 09/228,986
FRICH RILING DATE: 1999-01-12
FRICH RILING DATE: 1999-10-12
FRICH RILING DATE: 1999-10-11
FRICH PAPLICATION NUMBER: PCT/USO0/00724
FRICH RILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 902
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Patent No. 6159198

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 DKSLTTDSQSLGMGSI----NM----LLH------VSSRRTLDEEPNTI 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 -SWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 GLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV- 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 CNOSDVQALISFKQTVSSSSPLN----WEVNRSCCTWEGVTCGLLSLQQFSVTKLRLPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 CHHDDLHALRGLAENLSGKGAVRLRAAWS-GASCCSWEGVGCETASGR----VVALRLPKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 QGLNSIRTFNISSNSFRGNVPQLGSAVNLTSFNVSNNSFTG 191
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12.3%; Score 170.5; DB 3;
Best Local Similarity 26.1%; Pred. No. 8.9e-08;
Matches 81; Conservative 39; Mismatches 89;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.3%; Score 170.5; DB 4
32.3%; Pred. No. 3.8e-08;
iive 25; Mismatches 61
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; ORGANISM: Pinus radiata
US-09-228-986-80
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US-10-101-464A-902
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Matches 52; Conserv
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US-09-228-986-80
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------NNNHVSGSNNTVVTG-----SDNTVVGSNHVVSGTKHIVTDNNNV 221
                                      12.6%; Score 175; DB 27.1%; Pred. No. 4.5e tive 25; Mismatches
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OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                         126 TTDSQSLGMGSINMLLHVSS-----
                                                                                                                                                                                                                                                                                         230 SGSFHTVSGEH------
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Best Local Similarity 22.74
Matches 80; Conservative
                                                                                Conservative
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                                                          Local Similarity
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US-10-101-464A-893
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US-09-952-267B-15
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               --VSGND 226
                                               239 NCTSLTDLVISSNNLSGPIPSEFSGLVSLKFLFLDDNSISGSIPTSLVNCTSLFALKGSG 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 SGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTK--HIVTDNNNVVSGNDNNV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 LGNNATISGGRQNEASGDRSTVAGGEQNQAIGKYSTISGGRQNEASGDRSTVAGGEQNQA 303
                                                                                                                                                                                                                                       Sequence 15, Application US/09336447A

Sequence 15, Application US/09336447A

Patent No. 6310190

GENERAL INFORMATION:

APPLICANT: HANSEN, ERIC J.

APPLICANT: AEBI, CHRISTOPH

APPLICANT: OFFICENT: AEBI, CHRISTOPH

APPLICANT: PISKE, MICHAEL J.

APPLICANT: FREBENBURG, ROSS A.

TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS

FILE REPERBURG: AMCY:024

CURRENT APPLICATION NUMBER: US/09/336,447A

CURRENT APPLICATION NUMBER: 1999-06-21

NUMBER OF SEQ ID NOS: 98

SOFTWARE: PATENTING DATE: 1989-06-21
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBLI CHRISTOPH
APPLICANT: AEBLI CHRISTOPH
APPLICANT: ACIVER, LEGILE D.
APPLICANT: PISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBUG, ROSS A.
TITLE OF INVENTION: USPAI AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:0.24
CURRENT FILING DATE: 2010-09-12
PRIOR FILING DATE: 1999-06-21
PRIOR PLING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN OF: 2.1
SEQ ID NO 15
LENGTH: 889
TYPE: PRI
ORGANISM: MOTAXELIA CATAITHALIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 889;
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                                                                                                                           299 NKLSGPIPSVMGLMKSISTIDLSNNSLTG 327
                                                                                                 227 NNVSGSFHTVSG---EHNTVSGSNNTVSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-952-267B-15; Sequence 15, Application US/09952267B; Patent No. 6753417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Moraxella catarrhalis
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                   ---TGSDNTVVGSNHV----
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US-09-336-447A-15
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LENGTH: 889
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Sequence 893, Application US/10101464A

Faceurus 893, Application US/10101464A

Faceurus 893, Application US/10101464A

Faceurus 893, Application US/10101464A

GENERAL INPORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT FILING DATE: 2000-101.01

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR APPLICATION NUMBER: 09/228,986

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

SPRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

SPRIOR FILING DATE: 1999-11-01

SPRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

PRIOR FILING DATE: 1999-11-01

SPRIOR FILING DATE: 1999-01-12

SPRIOR FILING DATE: 1999-01-13

SPRIOR PRIOR PRIO
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                                                                                                                                                                                                                                                                                                                         172 SGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTK--HIVTDNNNVVSGNDNNV 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 LGNNATISGGRQNEASGDRSTVAGGEONQAIGKYSTISGGRQNEASGDRSTVAGGEONQA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | : |||| : |||| 304 IGKYSTVSGGYRNQATGKGSFAAGIDNKANADNAVALGNKNTIEGENSVAIGSNNTV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 KSLTTDSQSLGMGSIN----MLLHVSSRRTLDEEPNTISGT-NNSVGSGS-----
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22.7%; Pred. No. 5.2e-08;
ive 55; Mismatches 107; Indels 110;
; DB 4; Length 889; 4.5e-08;
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US-09-952-267B-5
                                                                                                                            SEQ ID NO 5
LENGTH: 892
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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APPLICANT: HANSEN, ERIC J.
APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: COPE, LESLIE D.
APPLICANT: FREDENBURG, MICHAEL J.
APPLICANT: FREDENBURG, NOSA.
TITLE OF INVENTION: USPAI AND USPAZ ANTIGENS OF MORAXELLA CATARRHALIS FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEC ID NOS: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
                                                                                                                                                                                                                                                                                                                                                                                                                                      ----NNQATGNGSFAAGVENKADANNAVALGNKNTIEGTNSVAIGSNNTVKTG 230
                                                                                                                                                                                                                                                                                                                                                                                                                 214 IVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG
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                                                                                                                                                                                                                                      13.1%; Score 182; DB 4; Length 941; llarity 34.2%; Pred. No. 1e-08; Conservative 19; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 892;
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CURRENT FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 9
LENGTH: 941
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                                                                                                                                                                    ; ORGANISM: Moraxella catarrhalis
US-09-952-2678-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
Matches 35; Conserval
                                                                                                                                                                                                                                                            Best Local Similarity
Matches 39; Conserva
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APPLICANT: Misuwenhuizen, Micolaas
APPLICANT: Misuwenhuizen, Micolaas
APPLICANT: Misuwenhuizen, Micolaas
APPLICANT: Higgins, Colleen M.
ITILE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 SGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLD 104
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6 LLLVMMGVAMPTHSQHTGGFTSVQRFPFNGRSMMGKPSIAGYHEKRDVEALLSFRKGITL
                                                                                                                                                                                                                                                                                                                                                                             Gaps
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9
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12.8%; Score 177; DB 4;
Best Local Similarity 31.8%; Pred. No. 2.9e-08;
Matches 35; Conservative 20; Mismatches 49;
CURRENT APPLICATION NUMBER: US/09/952,267B CURRENT FILING DATE: 2001-09-12 PRIOR APPLICATION NUMBER: US/09/336,447 PRIOR FILING DATE: 1999-06-21 NUMBER OF SEQ ID NOS: 98 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-10-101-464A-890
; Sequence 890, Application US/10101464A
; Patent No. 6768041
                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Moraxella catarrhalis
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APPLICANT: Strabala, Timothy
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Best Local Similarity 23.49
Matches: 77; Conservative
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ORGANISM: Pinus radiata
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US-09-336-447A-9
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Sequence 5, Appli
Sequence 5, Appli
Sequence 890, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
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Sequence 953, App
Sequence 770, App
Sequence 743, App
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764, App
902, App
80, Appl
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7, Appli
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Sequence 897,
Sequence 911,
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1385
1 MPEYMAKCCMLLVFLGFILQ........NTVSGSNHIVSGSNKVVTDG 267
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Sequence 6
Sequence 6
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-36-447A-15

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US-10-101-464A-893

US-10-101-464A-893

US-10-101-464A-802

US-09-22B-986-80

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US-09-22B-986-80

US-09-101-464A-902

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US-10-101-464A-914
US-09-345-473E-15
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Listing first 45 summaries
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79, Appl
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AEBL, CHRISTOPH
APPLICANT: AEBL, CHRISTOPH
APPLICANT: APPLICANT: ABEL, CHRISTOPH
APPLICANT: OFE, LESLIE D.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FISKEN, MICHAEL J.
APPLICANT: FISKEN, MICHAEL J.
APPLICANT: FISKEN, MICHAEL J.
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 9
LENGTH: 941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 NTISGTNMSVGSGSNMVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKA
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APPLICANT: HANSEN, ERIC J.
APPLICANT: AREBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MCHAEL J.
APPLICANT: FISKE, MCHAEL J.
APPLICANT: FISKE, MCHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TILE OF INVENTOR: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REPERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/952,267B
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US-09-345-473E-16
US-09-336-447A-13
US-09-5450-258-13
US-09-228-986-79
US-10-101-464A-79
US-10-101-464A-72
US-10-101-464A-932
US-10-101-464A-932
US-09-952-267B-1
US-09-952-267B-1
US-10-101-464A-944
US-10-101-464A-944
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US-10-101-464A-79
                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 9, Application US/09336447A; Patent No. 6310190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09952267B Patent No. 6753417
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Proc. Natl Acad. Sci. U.S.A. 101:13826-13831(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60; Gaps
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Brhartoideae; Oryzeae; Oryza.

[1]
                                                                                                                                                                                                                                                                        Yersinia pseudotuberculosis IP 32953.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 622;
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622 AA; 65230 MW; 30B8C7D77A3D73CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q75GM9;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein OSJNBa0018K15.10.
                                                                                                                                                              25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
229 LTVA--INNLQGLIPPVLFNMSSLECLNFGSNQLSGS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 194; DB 2; 26.8%; Pred. No. 3.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           917 AA
                                                                                                                 622 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEEPNTISGINNSVGSGSNNVVSGNDNTVVS-
                                                                                                                                                                                                                                   Putative exported protein precursor. ORFNames=YPTB1413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DANINGSNNYVIDG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; BX936398; CAH20653.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HI-VSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 26.8
nes 68; Conservative
                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=IP 32953;
PubMed=15358858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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SIGNAL
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                                                                       RESULT 14
Q66CJ0
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64 WEGVGCETASGRVVALRLPKRGLGGIIP-SSIGELDHLRYLDLSGNSLVGEVPKSLQIRL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 TNNSVGSG------SNNVVSGNDNTVVS------GNNNHVSGSNNTV--V 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 TGSDNTVVGSNHV-----VSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVS 244
                                                                                                                                                      Leu H.-L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 AKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWS--GASCCS
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Chow T.-Y. Hsing Y.-I.C., Chen C.-S., Chen H.-H., Liu S.-M.,
Chow T.-Y. Hsing Y.-I.C., Chen S.-J., Chen T.-Y., Hsing Y.-I.C., Chen S.-Y.,
Chen Y.-T., Lee P.-F., Chang S.-J., Chen H.-C., Chen S.-Y.,
Chen T.-R., Chen Y.-L., Cheng C.-H., Rau P.-I., Lee M.-C.,
Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
A. Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
A. Li Y.-P., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,
Chen L. Shaw J.-F.;
Chen J.-P.
Chen J.-C., Chen S.-Y.
Chen H.-C., Chen S.-Y.
Chen J.-C., Chen S.-Y.
Chen J.-P.
Chen J.-P.
Chen J.-P.
Chen J.-P.
Chen J.-C., Chen J.-P.
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Chen J.-C., Chen J.-P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.0%; Score 194; DB 2; 26.3%; Pred. No. 5.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 26.3% les 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 GSNNTVSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 LSGNALTG 296
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251 MSNNLSGEVPKSLFNTSSLTAIFLQQNSFVGSIPAIAAMSSPI----KYISLRDNCISGT 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 THGFCSWTGVECSSAHPGHVKALRLQGLGLSGTISPFLGNLSRLRALDLSGNKLQGQIPS 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 SL----QIRLKSLTTDSQS----LCMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 NVVSGNDNTVVSGNNNHVSG----SNNTVVTG---SDNTVVGSNHVVSGTKHIVTDNN 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Target very in the series of the barley D-hordein locus in comparison with its orthologous regions of wheat genomes.";

All Genome 46:1084-1097(2003).

-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

EMBL; AY268139; AAP31049.1; -..

EMBL; AY268139; AAP31049.1; -..

EMBL; AY268139; AAP31049.1; -..

EMBL; AY268139; AAP31049.1; -..

CO; GO:0004574; F: Protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F: Receptor activity; IEA.

GO; GO:0016740; F: Protein serine/threonine kinase activity; IEA.

GO; GO:0016740; F: Receptor activity; IEA.

InterPro; IPR001010; F: Receptor activity; IEA.

InterPro; IPR0011019; F: Receptor activity; IEA.

InterPro; IPR001101; F: Receptor activity; IEA.

InterPro; IPR001101; F: Receptor activity; IEA.

InterPro; IPR001101; F: Receptor activity; IEA.

RECEPTOR: PRO0101; F: Receptor activity; IEA.

RECEPTOR: RECEPTOR ACTIVITY RINASE DOM; I.

RECEPTOR: RECEPTOR ACTIVITY RINASE DOM; I.

RECEPTOR: RECEPTOR ACTIVITY RINASE DOM; I.

RECEPTOR ACTIVITY RECEPTOR ACTIVITY RINASE DOM; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 14.1%; Score 195.5; DB 2; Length 1023; l Similarity 30.3%; Pred. No. 5.2e-06; 84; Conservative 37; Mismatches 113; Indels 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PubMed=14663527; DOI=10.1139/g03-071;
Gu Y.O., Anderson O.D., Londeore C.F., Kong X., Chibbar R.N.,
Lazo G.R.;
                                                                                                                                                      307 IPESLGHIRTLEILTMSVNNLSGLVPPSLFNISSLTFLAMGNNSLV 352
                                                                                                           233 FHTVSGEHNTVS----GSNN-----TVSGSNHIVSGSNKVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1023 AA; 110187 MW; 09EB62D3C41141C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1023 AA
                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative receptor kinase
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                         Q84NG8;
01-JUN-2003
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | | | | | : | | | | | | | | SMNSLEGNIPSOLSSYSQIEILDLSSNSFQGAIPASLGKCIHLODINLSRNNLQGRISSA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNNHVSG-----SINNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 VFLGFILOVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASC--CSWEGVGCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 IFCSISLAICNET-----DDRQALLCFKSQLSGPS--RVLSSWSNTSLNFCNWDGVTCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SRSPPRVIAIDLSSEGITGTISPCIANLTSLMTLQLSNNSLHGSIPPKLGLLRKLRNLNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 MGSINML--LHVSSRRTLDEEPNTIS-----GTNNSVGSGSNNVVSGNDNTVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.2%; Score 196; DB 2; Length 1102;
24.3%; Pred. No. 5.2e-06;
ive 47; Mismatches 109; Indels 106; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Subjected Nove-2002 to the Embly Geneauk/Debo databases.

REMEL, AP005966; BAD34184.1; -
COUNTY OF COUNTY C
   Oryza sativa (japonica cultivar-group).
Wkaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sasaki T., Matsumoto T., Katayose Y.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Hypothetical_protein; Kinase;
Serine/threonine-protein kinase; Transferase.
SEQUENCE 1102 AA; 119984 MW; B960CDE45175C68E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                             25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypotherical protein B1047H05.16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 TAS-GRVVALRLPKRG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 24.3%;
Matches 84; Conservative 4
                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=39947;
                                       230
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119 -QIRLKSLTTD-----SQSLGMGSINMLLHVSSRRTLDBEPNTISGTNNSVGSGSNNVV 171
                                                                  SGNDNTVVSGNNNHVSG-----SNNTVVTGSDNTVVGS--NHVVSGTKHIVTDNNNVVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Cheuk R., Chen H., Kim C.J., Shinn P., Bowser L., Carninci P., Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Huuan V.W., Ishida J., Jones T., Kamiya A., Kazlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Palm C.J., Lam B., A Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., A Toriumi M., Wallander E.K., Wong C., Wu H.C., Yamada K., Yu G., Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

Shall, BABO2561; BAB03647.1; ---
RMBL, BAD0364; P:ATP binding; IEA.

GO; GO:0004672; F:ATP binding; IEA.

GO; GO:0004672; F:receptor activity; IEA.

GO; GO:000468; P:procein maino acid phosphorylation; IEA.

InterPro; IPR001091; IRR plant.

RINEERPO; IPR001091; IRR plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 CSWRGVTCDASSRHVTVLSLPSSNLTGTLPSNLGSLNSLQRLDLSNNSINGSFPVSLLNA
                                                                                                         | : | | : | | : | | : | | 175 ----TEISLQKNYLSGGIPGGFKSTEYLDLSSNLIKGSLPSHFRGNRLRYFNASYNRIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172 SGNDNTVVSGNNNHVSG-----SNNTVVTGSDNTVVGS--NHVVSGTKHIVTDNNNVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 CSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 TELRFLDLSDNHISGALPASFGALSNLOVLNLSDNSFVGELPNTL-GWNRNL-----
124 TELRFLDLSDNHISGALPASFGALSNLQVLNLSDNSFVGELPNTL-GWNRNL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 G------NDNNVSGSFHTVSG------EHNTVSGSNNTVSGSNH 255
                                                                                                                                                                                                    ------HNINVSGSFHTVSG------EHNTVSGSNNTVSGSNH
                                                                                                                                                                                                                                              GEIPSGFADEIPEDATVDLSFNQLTGQIPGFRVLDNQESNSFSG-NPGLCGSDH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Kaneko I., Katoh I., Katoh E., Sato S., Nakamura Y., Kotani
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Pred. No. 2.5e-06;
4; Mismatches 78; Indels 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     751 AA; 82062 MW; 180302F2B7EFF966 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation updat
Receptor-like protein kinase (At5g67280/K3G17_4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                        751
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PRINTS; PR00019; LEURICHRPT.
ProDom; P0000001; Prot Kinase; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
Kinase; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1999)
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SEOUENCE FROM N.A.
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                                                                                                                                        175
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                                                                  172
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Q9FGQ5
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DATA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QIRLKSLTTD-----SQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNVV 171
                                                                                                                                                                                                                                                                                                                 189
                                                                                                                                                                                                        59 KTTDCCSWDGVTCDDKSGQVISLDLRSTLLNSSLKTNSSLFRLQYLRHLDLSGCNLHGEI 118
                                                                                                                                            90
                                                                         28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Labowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Phanm P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFRIFFNNFTSLPSD-----LSGFHNLVTFDISA-----NSFSGHFPKFLFSIPSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----NNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHT-----
                                                           ---QRDGLLKFRDEFPIFESKSSPWN
                                                                                                                                                                                                                                                                              PSSIGELDHLRYLDLSGNSLVGEVPKSL----OIRLKSLTTDSQSLG-----MGSINMLL
                                                                                                                                                                                                                                                                                                                                                                                                                142 HVSSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
AT5g67280/X3G17 4.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantue; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
          CMLLVFLGFIL-QVAGATSWSCHHDDLHALRGLAENLSGKGAVRLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AUG-2001) to the EMBL/GenBank/DDBJ databases
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ProDom; PD000001; Proct Kinase; 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSING 751 AA; 82086 WW; EGADAB4370F49689 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.3%; Score 197.5; DB 2; 28.6%; Pred. No. 2.5e-06; iive 34; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | | : | | | : : | : | : | : | : | AWVSMDRNQFSG---PIEFAN--ISSSSKL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -- VSGEHNTVSGSNNTVSGSNHIVSGSNKV 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           751
                                                                                                                                            58 GAS-CCSWEGVGCETASGRVVALRLPKR---
                                                    |:: :: |:: :| | || CIITIYFSFLIHSLASPSLHFCRHD----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR007090; LRR plant.
InterPro; IPR000719; Prot_kinase.
Pfam; PF00560; LRR_1; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 28.6%
les 67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ecker J.R.;
Submitted (
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                                                                                                                                                                                                                                                                              91
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Best Local Similarity
Matches 80; Conserv
                                                                                                                          Local Similarity
                                                                          Kinase; Receptor
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                                                                                     SEQUENCE
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                       156
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                                                                                                                                      Matches
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                                   14;
                                                                                                                             58 -GASCCSWEGVGCETA-----SGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLS 106
                                                                                                                                                                 GNSLVGEVPKSL----QIRLKSLTTDSQSLGMGSINMLLHVSSRRTLDBEPNTISG---- 158
                                                                                                                                                                               --TNN-----SVGSGSNNVVSGNDNTV--VSGNNNHVSG-----SNNTVV 194
                                                                                                                                                                                                                                  SLCNNLPRIREIDLAMNYFDGSIPVGIGNCSSVEYLGLASNNLSGSIPQELFQLSNLSVL 235
                                                                                                                                                                                                                                                                      TGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTV-----SGEHNTVS 244
                                                                                                                                                                                                                                                                                      236 ALQNNRLSGA----LSSKLGKLSNLGRLDISSNKFSGKIPDVFLELNKLWYFSAQSNLFN 291
                                                                          8 VILILVGFCVQIVVVNSQNLTCNSNDLKALEGFMRGLESSIDG------WKWNESSS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
He G.M., Li K.G., Yang J.S.;
He G.M., Li K.G., Yang J.S.;
"Oryza sativa (Indica cultivar-group) chromosome 2 genomic sequence.";
Submitted (ANG-2004) to the EMBL/GenBank/DDBJ databases.
                                                           10 MLLVFLGFILQ--VAGATSWSCHHDDLHAL----RGLAENLSGKGAVRLRAAWS----
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putative leucine-rich repeat receptor-like kinase.
Oryza sativa (indica cultivar-group).
Sukaryota, viridiplantae; Streptophyra, Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUELEAF;
ISOURTHOUS, Yang J.S.;
Isolation and expression pattern of putative LRR (leucine-rich repeat) receptor-like kinase in rice.";
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY130046; AAU12611.1;
EMBL; AY14494; AAU12603.1;
GO; GO:0016301; F:kinase activity; IEA.
GO; GO:000487; F:receptor activity; IEA.
InterPro; IPR011009; Kinase_like.
                                   98;
         Length 1021;
                                  94; Indels
       14.7%; Score 204; DB 1; 24.6%; Pred. No. 1.2e-06; ive 56; Mismatches 94
                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1065 AA.
                                                                                                                                                                                                                                                                                                                       .----NNTVSGSNHI 256
                                                                                                                                                                                                                                                                                                                                      292 GEMPRSLSNSRSISLLSLRNNTLSGQIYL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003885; IRR_cyst.
InterPro; IRR007090; IRR_plant.
InterPro; IPR000719; Prot kinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR008271; Ser_thr_pkin_AS.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00560; LRR 1; 20
Pfam; PF00560; LRR 1; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00019; LEURICHRPT.
ProDom; PD000001; Prot kinas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD000001; Prot_kinas
SMART; SM00365; LRR_SD22; 6.
                                  81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                       ----S5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_TaxID=39946;
                                                                                                                                                                                                                                                                                                                       245
          Query Match
                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                           Q66QA4;
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183 EMMKNIJVMINASNINSFTGQIPSNFCSRSPSLTVIJALCYNHINGSIPPGFGNCIKLRVLKA 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 KSLQIRLKSLTTDSQSLGMGSINML-------LHVSSRRTLDEEPNT-- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----ISGTNNS-VGSGSNNVVSGNDN-TVVSGNNNHVSGS------NNTVVTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243 GHNNLSGNLPGDLFNATSLEYLSFPNNELNGVINGTLIVNLRNLSTLDLEGNNINGRIPD 302
                                                                                                                                                                                                                                                                                                                                                                               7 KCCMLLVFLGF------ILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                SDNTVVGS-----DNNNV-----KHIVTS-----KHIVTS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>`</u>
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 SIGQLKRLQDLHLGDNNISGELPSALSNCTHLITINLKRNNFSGNLSNVNFSN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----VSGNDNNVSGSF------H--TVSGEHNTVSGSNNTVSGSN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu
maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.4%; Score 199.5; DB 2; Length 784; 24.2%; Pred. No. 1.9e-06; ive 51; Mismatches 80; Indels 119
                                                                                                                                                                                                                                                          14.5%; Score 201; DB 2; Length 1065; 24.6%; Pred. No. 2.1e-06; ive 54; Mismatches 98; Indels 114
                                                                                                                                                                                                     1065 AA; 116827 MW; CFE570663C05BF0A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
protein; 69620-67266.
                                                                                      UNKNOWN 1
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SMART; SM00369; LRR_TYP; 8.
SMART; SM00220; S_TKc; 1.
SMART; SM00219; TYTKC; 1.
PROSTIF; PS001107; PROTEIN KINASE ATP; UN
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN KINASE_DOM; 1.
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Town C.D., Kaul S.;
Submitted (JAN-2001) to the EMBL/
BMEL, AC016163; AAG51813.1; -.
InterPro; IPR001611; LRR.
InterPro; IPR0090; LRR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative disease resistance
Name=F26A9.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam, PF00560; LRR 1; PR00560; LRR 1; PR00560; LBURICHRPT. SEQUENCE 784 AA; 88730 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80; Conservative
                                                                                                                                                                                                                                                                                                                      87; Conservative
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N-linked
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                                                                                                                             EMBL; AB060167; BAC00995.1; -. HSSP; Q62838; 1LUF.
                                                                                                                                                                                                                                                                                                                                                                                                                       555
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629
1014
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771
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SIGNAL
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STREET TO THE TOTAL TO THE TOTA
                                                                                                                                                                                                                          85 GLGGIIPSSIG-ELDHLRYLDLSGNSLVGEVPKSLQ....-IRLK-SLTTDSQSLGMG 135
                                                                                                                                                                                                                                                                                                                                        136 SINML--LHVSSRRTLDEEPNTISGTNN--SVGSGSNNVVSGNDNTVVSG------ 181
                                                                                                                                                                                                                                                                                                                                                                                                         ----SNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG 224
                                                                                                                                                                                                                                                                                                                                                                                                                            6 FIMPLVVISVLTICESKACHPDDLKGLNDFKVGIHSDTSGR----LSNWKGTECCNWPG 60
                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daucus carota (Carrot).
Eukaryoca; Vitidiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Apiales; Apiaceae; Apioideae; Scandiceae; Daucinae;
                                                                                                                                                                                                                                                                                                                                                       14 FLGFILQVAGAT---SWSCHHDDLHALR----GLAENLSGKGAVRLRAAWSGASCCSWEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         meristem, hypocotyl and root.

PTM: N-glycosylated.

MISCELLANEOUS: A 36 amino-acid island is present in the 18th
leucine-rich repeat. An island domain has also been found among
the extra-cellular LRRs of the brassinosteroid receptor BRI1 and
has been shown to be critical for its function.

SIMILARITY: Belongs to the Ser/Thr protein kinase family.
SIMILARITY: Contains 21 leucine-rich (LRR) repeats.
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., FUNCTION, TISSUE SPECIFICITY, AND GLYCOSYLATION MEDLINE=22025707; PubMed=12029134; DOI=10.1126/science.1069607; Matsubayashi Y., Ogawa M., Morita A., Sakagami Y.; "An LRR receptor kinase involved in perception of a peptide plant bormone, phytosulfokine."; Science 296:1470-1472(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Phytosulfokine receptor precursor (EC 2.7.1.37) (Phytosulfokine LRR receptor kinase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: Receptor with a serine/threonine-protein kinase activity. Regulates, in response to phytosulfokine binding, a signaling cascade involved in plant cell differentiation, organogenesis and somatic embryogenesis.

-i- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.

-i- SUBCELLULAR LOCATION: Type I membrane protein; plasma membrane
                                                                                                 90; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similarity)
TISSUE SPECIFICITY: Expressed ubiquitously in leaf, apical
                                                                   Length 353;
                 21 Potential.
38363 MW; 44CEA54EE2595COF CRC64;
                                                               15.3%; Score 212; DB 2; 24.2%; Pred. No. 8.1e-08; iive 50; Mismatches 90,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1021 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 297 LPNSICGT----SGLSVLFISHNKIVG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 NDNNVSGSFHTVSG-----EHNTVSG 245
                                                                                                                                                                                                   67 VGCETASGRVVALRLPKR-----
                                                 Ouery Match
Best Local Similarity 24.2%
Best Local Similarity 24.2%
                                                                                                                                                                                                                                                                                                                                                                                                            NNNHVSG-----
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353 AA;
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                                   SEQUENCE
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   Signal.
SIGNAL
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). M. TherPro; IPR011009; Kinase_like.

R. InterPro; IPR01101; LRR.

R. InterPro; IPR00161; LRR.

R. InterPro; IPR000709; LRR.plant.

R. InterPro; IPR000719; Prot_kinase.

R. Ffans, PF00060; LRR; 16.

R. Pfan; PF00060; Prot_kinase; 1.

R. PROSTE; PF000109; Prot_kinase; 1.

R. ROGITE; PF001019; PROTEIN KINASE ATP; 1.

R. ROSITE; PF001019; PROTEIN KINASE ST; 1.

R. ROSITE; PF001019; RROTEIN KINASE ST; 1.

R. ATP-binding; Glycoprotein; Kinase; Leucine-rich repeat; Receptor; M. Repeat; Receptor; M. Repeat; Renamenhyane.

R. Athenmenhyane.

R. Ath (Potential). (Potential). (Potential). (Potential) (Potential) (Potential) (Potential) (Potential) (Potential) (Potential) inked (GlcNAc. ..) (Potential) B0C7F101B29144C2 CRC64; (Potential) Potential) (Potential) Potential) Potential Potential similarity) Potential. Phytosulfokine receptor. Potential. acceptor (By similarity) (By similarity) (By similarity) (atypical). (GlcNAc. (GlcNAc. (GlcNAc. (GlcNAc. (GlcNAc. lcNAc. (GlcNAc lcNAc (GlcNAc LCNAC (GlcNAc LCNAC 1cNAc LCNAC lcNAc CNAC LRR 2.
LRR 3.
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LRR 18.
LRR 19.
LRR 19.
LRR 20.
LRR 20 <u>6</u>6 N-linked N-linked 112098 MW; A, 546 568 576 592 632 SEQUENCE m

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PRINTS; PR00019; LEURICHRPT.
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Matches 55; Conserv
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                                                                                                                                                                                                                                                                                                                                                                         A Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
A Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sabahia M., Thomson N.R., Bason N., Basocham I.R.,
Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
A Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
A Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
A Rabbinowitsch E., Rutherford K., Sanders M., Simmonds M.,
A Songaiviai S., Stevens K., Tumapa S., Vesaratchavest M.,
Mhitchead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
T. "Genomic plasticity of the causative agent of melioidosis,
Burkholderia pseudomallei.", 101:14240-14245(2004).
E. EMBL, BX571965; CAH35630.1;
CREMBL, BX571965; CAH35630.1;
CREMBL, BX571965; CAH35630.1;
CREMBL, BX571965; CAH35630.1;
CREMBL, BX571965; CAH35630.1;
CREGE T. T. CREMBL, TANA, TOUR T. WALL AGENT T. CREMBL, BX571965; CAH35630.1;
CREMBL, BX571965; CAH35630.1;
CREMBL, BX571965; CAH36530.1;
CREMBL, BX571965; CAH36530.1;
CREMBL, BX571965; CAH36530.1;
CREMBL, CAMBL, CAMBL
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STRAIN=ATC2 23344;
Nierman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.E.,
Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPSSIGELDHLRYLDLSGNSLVGEVPKSLQ-----IRLKSLTTDSQSLGMGSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 TPVLLTNVAAGKIAATSTDAVNGSQLYTLQQEFSQQYDLLTSQVSSLSTSVSGL-QGSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             481 -ATGTDSTASGSNSTANGTNSTASGDNSTASGTNASATGENSTATGTDSTASGSNSTANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36 ALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGCETASGRVVALRLPKR-----GLGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 VVTGSDNTVVGS------NHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSG
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Burkholderiaceae; Burkholderia.
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27.7%; Pred. No. 6.6e-08;
ive 41; Mismatches 99
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                                                                                                                                                Burkholderia pseudomallei K96243.
                                                                                          Putative outer membrane protein.
                                                                                                                                                                                                       Burkholderiaceae; Burkholderia
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25-OCT-2004 (TrEMBLrel. 28,
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25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
25-OCT-2004 (TrEMBLrel.
                                                                                                                                                                                                                                        NCBI_TaxID=272560;
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                     ORFNames=BPSL1631
                                                                                                                                                                                                                                                                                                                            STRAIN=K96243;
PubMed=15377794;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 VSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Agendicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Petunia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:| : : | |: | : | | : | | | SGDSSTASGTNASATGENSTATGTDSTASGSNSTANGTNS--TASGDNSTASGTNASATG
                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R., Mohammoud Y., Nelson W.C., Radune D., Romero C.M., Sarria S., Selengut J., Shambin C., Sullivan S.A., White O., Yu Y., Zafar N., Zhou L., Fraser C.M.; "Structural flexibility in the Burkholderia mallei genome."; Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
                                                                                                                                                                                                                                                                                                                                                                                                           20;
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Guyon V., Tang W.H., Monti M.M., Raiola A., Lorenzo G.D.,
McCormick S., Taylor L.P.;
"Antisense phenotypes reveal a role for SHY, a pollen-specific
                                                                                                                                                                                                                                                                                                                                   Length 1012;
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                                                                                                                                                                                                                                                                                                                                                                                                       72; Indels
                                                                                                                                                                     Proc. Natl. Acad. Sci. .....

EMBL; CP000010; AAU48866.1; -. CPONTENCE 1012 AA; 94758 MW; 53C27D16C62FBBDE CRC64;
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Plant J. 39:643-654(2004).
EMBL; AF049920; AAD02546.2; -.
EMBL; AF325673; AAK11220.1; -.
INTERPO; IPR001611; LRR.
InterPro; IPR007090; LRR_plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Last Sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) PGPS/D4 precursor (LRR protein S/D4).
                                                                                                                                                                                                                                                                                                                                                                     ; Pred. No. 1.1e-07;
31; Mismatches 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                  30.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petunia hybrida (Petunia).
                                                                                                                                                                                                                                                                                                                                                                                                           55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 EGVGCETASGRVVALRIPKRGLGGIIPSSIGELDHIRYLDLSGNSLVGEVPKSLQIRLKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            125 LTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGT-----NNSVGSGSNNVVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 KCCML-LVFLGFILQVAGATSWSCHHDDLHALRGLAENLS-GKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 5. III. Sequence features of the regions of 1,191,918 bp covered by seventeen physically assigned P1 clones.";

DNA Res. 4:401-414(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative receptor protein kinase.

Name-At5953800,

Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magplantae; Streptophyta; core eudicots; rosids;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
RN (1)

RP SEQUENCE FROM N.A.

RA Saash I., Matsumnoto T., Yamamoto K.;

RT "Cryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC

RT "Clone:P0585H11.";

RT Clone:P0585H11.";

RT Clone:P0585H11.";

RT Clone:P0585H11.";

RMEL, AP004342: BAC20742.1;

BRBL; AP004342: BAC20742.1;

BRBL; AP004342: BAC20742.1;

BR GO; GO: 00004674: Fire binding; IEA.

BR GO; GO: 00004674: Fire binding; IEA.

BR GO; GO: 00004674: Fire estine/thronine kinase activity; IEA.

BR GO; GO: 00004674: Fire estine/thronine kinase activity; IEA.

BR GO; GO: 00004674: Fire estine/thronine kinase activity; IEA.

BR GO; GO: 00004674: Fire estine/thronine kinase activity; IEA.

BR GO; GO: 00004674: Fire estine/thronine kinase activity; IEA.

BR GO; GO: 00004872: Fire estine/thronine kinase activity; IEA.

BR GO; GO: 00004872: Fire estine/thronine kinase;

BR GO; GO: 00004872: Fire estine/thronine-protein kinase;

BR Fam; PF00069: PRINTER PROTEIN KINASE ATP; 1.

BR PROSITE; PS00107: PROTEIN KINASE ST; 1.

BR PROSITE; PS00107: PROTEIN KINASE ST; 1.

BR TARP-binding; Kinase; Receptor; Serine/threonine-protein kinase;

KW Transferase.

BR SEQUENCE 1010 AA; 109074 MW; 5CCB04ESIEIBAFO2 CRC64;
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MEDLINE=98162728; PubMed=9501997;
Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
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Last annotation update)
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18.9%; Score 262; DB 2;
Best Local Similarity 40.1%; Pred. No. 5.5e-11;
Matches 71; Conservative 19; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1036 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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SECUENCE FROM N.A.
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CE--TASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSL----QIRL 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | : | | : | | : | | 229 | 174 EIHPELCSSSGGIQVLDLSMRLVGNLD----GLYNCSKSIQQLHIDSNRLYGQLPDYLY 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW-SGASCCSWEGVG 68
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R EMBL; AB007644; BAB10719.1; -...
R EMBL; AV064019; AAA136375.1; -...
R EMBL; AV064019; AAA136375.1; -...
R EMBL; AV061800; AAA14119.1; -...
R GO; GO:00005224; F:ATP binding; IEA.
R GO; GO:0004672; F:receptor activity; IEA.
R GO; GO:0016740; F:transferase activity; IEA.
R GO; GO:0016487; F:receptor activity; IEA.
R GO; GO:001648; P:protein amino acid phosphorylation; IEA.
R InterPro; IPR001611; LRR. Plant.
R InterPro; IPR007090; LRR. Plant.
R InterPro; IPR00719; Prot kinase.
R InterPro; IPR006019; Prot kinase.
R InterPro; IPR00609; Primase: I...
R Pfam; PF00560; LRR. 1; Ser_thr_pkin_AS.
R Pfam; PF00560; Primase: I...
                                                                                                                                                                                                                                                                                                                                                                         Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones J.
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
Sakurai T., Satou M., Saki M., Shinn P., Southwick A., Shinozaki P.
Davis R.W., Ecker J.R., Theologis A.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1036 AA; 114339 MW; 6DF9511FC2A4E261 CRC64;
                                                                                                                                                                                                                                                                               Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
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ProDom; PD00001; Prot kinase; 1.
PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00111; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89; Conservative
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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Q63UH1;
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oryza sativ oryza sativ moraxella c oryza sativ aegilops ta arabidopsis oryza sativ arabidopsis oryza sativ oryza sativ oryza sativ oryza sativ arabidopsis arabidopsis

Q6z3t9 Q67it2 Q9xd54 Q6et59 Q9m9x1 Q91gi5 Q6r2j8 Q6r2j3 Q6r2j3 Q6r2j3 Q6r2j3

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150 DEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DEQPNTISGSNNTVRSGSKOVILAGNDNTVISGDNNSVSGSNNTVVSGNDNTVTGSNHVVS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GTNHIVTDNNNVSGNDNNVSGSFHTVSGGHNTVSGSNNTVSGSNHVVSGSNKVVTD 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 GTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTJVSGSNHIVSGSNKVVTD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAÏN <1 118 ice recrystallisation inhibition protein.
SEQUENCE 118 AA; 11766 MW; 0362C1E4F98AE9F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 15, Last annotation update)
10-JUN-2003 (TrEMBLrel. 24, Last annotation update)
11-JUN-2003 (FremInial restriction inhibition protein (Fragment).
12- Lolium perenne (Perennial ryegrass).
13- Rukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
13- Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
14- Poeae; Lolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38.3%; Score 530; DB 2; Length 11
85.5%; Pred. No. 3.5e-32;
tive 10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sidebottom C.M.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ277399; CAB87814.1; -.
PDB; 113B; Model; A=1-118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Putative phytoaulfokine receptor.
Name=P0585H11.109;
                                                                                                                                                                                                                                                                                                                                           118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1010 AA
                                                                                                                                                                                                                                                              ALIGNMENTS
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             Q6Z3T9
Q67IT2
Q9XD54
Q6ET59
Q8LKV9
Q9LGI5
Q9LGI5
Q6R2J8
Q6R2J19
Q6R2J19
Q6R2J19
Q6R2J19
                                                                                                                                                                                                                                                                                                                                           PRT;
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Thesis (1999), University of York.
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                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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836
380
1051
941
718
653
883
1065
703
998
1047
1080
983
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             NCBI_TaxID=4522;
184.5
183.5
183.5
182.
181.5
181.
181
181
180.5
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Q9M3W4;
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09fh3y
06fh3y
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Q940M7
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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A;Gene: F19I3.16; At2g34930
A;Map position: 2
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R.Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaulsubmitted to the EMBL Data Library, April 1998
A;Reciption: Arabidopsis thaliana chromosome II BAC F1913 genomic sequence.
A;Reference number: 214160
A;Accession: T00475
A;Accession: T00475
A;Accession: T00475
A;Residues: L-905 <ROU7
A;Residues: 1-905 <ROU7
A;Residues: 1-905 <ROU7
A;Residues: 1-905 <ROU7
A;Cross-references: UNIPROT.064757; EMBL:AC004238; NID:g3033373; PID:g3033389
A;Residues: 1-905 <ROU7
A;Cross-references: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzbrey, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
      A;Cross-references: UNIPROT:022178; EMBL:AC002391; NID:g2642427; PID:g2642433
R;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rouneley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Ayture 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A64420; MUID:20083487; PMID:10617197
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A; Status: preliminary
A; Morecele type: DNA
A; Molecule type: DNA
A; Residues: 1-77 < 470>
A; Cross-references: GB: AE002093; NID: g2642433; PIDN: AAB87101.1; GSPDB: GN00139
C; Genetics:
A; Genetics:
A; Map position: 2
A; Introns: 545/1
C; Superfamily: protein kinase homology
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A;Molecule type: DNA
A;Residues: 1-905 <STO>
A;Cross-references: GB:AE002093; NID:g3033389; PIDN:AAC12833.1; GSPDB:GN00139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           147 HNL-----QTLNLSDNIFTGKLPA-----NLASLGSLTEVSLKNNYFSGEFPGGGWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 11.7%; Score 162; DB 2; Length 773; Local Similarity 27.3%; Pred. No. 0.00028; les 66; Conservative 36; Mismatches 86; Indels
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                                                                                     10 MLLVFLGFILQVAGATSWSCHHDDLHAL---RGLAENLSGKGAVRLRAAWSGASCCSWEG
                                          Gabs
                                          Indels 143;
                                                                                                                                                                                  67 VGCETASGRVVA--LRLP------KRG--LGGI------
                                          45; Mismatches 105;
11.7%; Score 161.5; DB 2; 23.1%; Pred. No. 0.00037;
                                                                                                                                                                                                                                                                       90 IPSSIGELDHLRYLDLSGNSLVGEVPKSL----
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                     Local Similarity 23.1% tos 88; Conservative
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R.; De

К. Е.

Mewes, H.W.; Mayer,

Ι.;

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probable receptor-like protein kinase At2923300 [imported] - Arabidopsis thaliana NiAlternate names: protein kinase homolog T20D16.7 (Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Arabidopsis thaliana (mouse-ear cress) (C.Species: Ol-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Aug-2004 (C.Accession: T00502, A84623 (R.R., Ketchum, K.A., Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kausubmitted to the EMBL Data Library, November 1997 (A.R., Arabidopsis thaliana chromosome II BAC T20D16 genomic sequence. A,Reference number: 214164 (A.R., A.R., Accession: T00502 (A.R., A.R., A.
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A;Introns: 863/1; 1116/1
A;Note: F1C12.60; F18F4.240
C;Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology;
                                                                                                                                                                                                                   hypothetical protein F18F4.240 - Arabidopsis thaliana NyAlternate names: hypothetical protein F1C12.60
NyAlternate names: hypothetical protein F1C12.60
Cypecies Arabidopsis thaliana (mouse-ear cress)
CyDate: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
CyAccession: T05322; T04898
CyAccession: T05322; T04898
Ews. M. M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1998
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         203 GYSLQYLNVSFNQISGEIPPEIGVNFPRNVTVDLSFNNLTG 243
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A,Residues: 1-1222 - BEBV>
A,Fesidues: 1-1222 - BEBV>
A,Experimental source: UNIPROT:Q9SN91; EMBL:AL022224
A,Experimental source: cultivar Columbia; BAC clone F1C12
K,Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Banoroft,
submitted to the Protein Sequence Database, February 1998
A,Reference number: 215388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-305 <BEW>
A;Cross-references: EMBL:AL021637
A;Experimental source: cultivar Columbia; BAC clone F18F4
C;Genetics:
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Pred. No. 0.00045;
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25.3%;
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Matches 71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z15408
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A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: T05322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Decies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C;Accession: B85440
R;anonymous, The Buropean Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: B85440
A;Restdues: preliminary
A;Molecule type: UNA
A;Restdues: 1-766 ASTO>
A;Cross-references: UNIPROT:023161; GB:NC_001268; NID:g7270708; PIDN:CAB80391.1; GSPDB:G
C;Genetics:
A;Gene: A74937250
A;Map position: 4
C;Superfamily: protein kinase homology
                                                                                                ij
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
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llarity 28.5%; Pred. No. 0.0002;
Conservative 35; Mismatches 67
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Best Local Similarity 27.4%;
Matches 63; Conservative 34
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Best Local Similarity
Matches 63; Conserv
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Chacession: George monoquemoc_revision oz-mai-zour #text_cnange O9-Jul-2004
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., Nature, N.F.; Hughes, B.; Huzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Lu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Hitles: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Dates: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: H84421
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: UNIPROT: Q9C699; GB: AEO05173; NID: 910092530; PIDN: AAG12927.1; GSPDB:
                                                                                                                                                                                                                                                                                                                    probable disease resistance protein, 3954-7013 [imported] - Arabidopsis thaliana
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138 SALDQLL-----VLDLSYNSFKGELPLQQSFGNGSNGIFPIQTVDLSSNLLEGEILSSS 191
                                                                                                                                                                                                                                                                                                                                                         C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                         NNHVSGSNNTVVTGSDNTVVGS 204
                                                                                                                                               VFLQGAFNLTSFNVSNNSFTGS
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Best Local Similarity 23.2%
Matches 84; Conservative
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A; Residues: 1-1019 <STO>
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Cispecie: Arabidopsis thaliana (mouse-ear cress)
Cispecie: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
Cispecession: G96746
Cispecession: G96746
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hunghes, B.; Huizar, J.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J. Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Retule: preliminary
A;Rolecule type: DNA
A;Retule type:
                                                                                                                                DNA Res. 8, 205-213, 2001
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And A,Reference number: ABI807; MUD:21595285; PMID:11759840
A,Status: preliminary
A,Status: preliminary
A,Facteus: preliminary
A,Facteus: DNA
A,Residues: 1-420 «KUR»
A,Coss-references: UNIPROT:Q8YZQ1; GB:BA000019; PIDN:BAB72364.1; PID:g17129751; GSPDB:GGGenetics: all0406
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                                                                     ;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguci
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---DNTVV-----SGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS 223
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           14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 GNDNNVSGSFHTVSGEHNTVSGSNNTVSGS-NHIVSGSNKVVTDG 267
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Best Local Similarity
Matches 58; Conserv
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C; Genetics:
A; Gene: T9N14.20
A; Map position: 1
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Best Local S
Matches 52
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Gaps

87

---GNNN 184

235

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probable protein kinase [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (Gouse-ear cress)
C;Species: Arabidopsis thaliana (Gouse-ear cress)
C;Species: Arabidopsis thaliana (Gouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: B86440
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: B86440
A;Accession: B86440
A;Accession: Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9C867; GB:AE005172; NID:g11054670; PIDN:AAG27890.1; GSPDB:
C;Genetics:
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ARE1857
Appothetical protein all0406 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 GEIPFSLGTLSHLTFLDLSENKLVGQVPSSIGNLTKLMYLRLSINHLSGKS-SVSFANLT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 -W--SGASCCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TINNSVGSGSNNIVVSGN--DNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSG 210
                                                                                                           GIIPSSIGELDHLRYLDLSGNSLVGEVPKS------LQIRLKSLTTDSQSLGMGSIN 138
                                                                                                                                                                                                                                                                                 130 KLIQLDIKEN-DFEPELIPDMSRFHNLEGFGGGNFFGPFFTSLFTIPSLRWVNLRDSNNN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 OWRPEDPDPCNWNGVTCDAKTKRVITLNLTYHKIMGPLPPDIGKLDHLKLLMLHNNALYG 111
                                6 MKSCCSWLLLISLLCSLSNESQ------AISPDGEALLSFRNAVTRSDSFIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 EVPKSL-----QIRLKS-LTTDSQSLGMGSINMLLHVSSRRTLDBEPNTISG----
                                                                                                                                                                                                                                                                                                                                                                      ---HVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVV--SGNDNNVSGSFHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAA--
                                                                                                                                                                                                                          139 MLLHVSSRRTLDEEPNTI ---SGTNNSVGSGSNNVVSGNDNTVVS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              211 TKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
12.5%; Score 173.5; DB 2
Best Local Similarity 24.7%; Pred. No. 2.8e-05;
Matches 70; Conservative 44; Mismatches 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-590 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A, Map position: 1
                                                                                                              88
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C; Species: Arabidopsis thaliana (Mouse-ear cress)
C; Species: Orabidopsis thaliana (G) Sebello (G) Arcession: C84633
R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID:20083487; PMID:10617197
A; Accession: C84633
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-743 cSTO>
A; Cross-references: UNIPROT:09ZUH7; GB:AE002093; NID:g4115376; PIDN:AAD03377.1; GSPDB:GN
C; Genetics:
A; Gene: At-2924160
A; Map position: 2
                                                                                                A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUD:20083487; PMID:10617197

A;Recession: G84524

A;Accession: G84524

A;Molecule type: DNA

A;Residues: 1-983 <STO>
A;Coss-references: UNIPROT:Q9ZUK3; GB:AE002093; NID:g4115363; PIDN:AAD03365.1; GSPDB:GN

A;Genetics:
A;Gene: At2g15080

A;Map position: 2
Ribin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R.; Koo, H.; Modelfat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 ESWTNNSDCCYWDGIKCDAKFGDVIELDLSFSCLRGQLNSNSSLFRLFQLRFLTTLDLSN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                             Length 983;
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                                                                                                                                                                                                                                                                                                                                                                                                                          13.0%; Score 179.5; DB 2; 21.7%; Pred. No. 1.9e-05; iive 56; Mismatches 113;
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12.7%; Score 176.5; DB 2
Best Local Similarity 26.7%; Pred. No. 2.3e-05;
Matches 63; Conservative 35; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 AAWSGAS-CCSWEGVGCETASGRVVAL-
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Best Local Similarity
Matches 81; Conserv
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13;

Gaps

79;

Indels

243

Length 590;

204

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R;Delseny, M.; Berger, C.; Cooke, R.; Grellet, F.; Laudie, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23013
A;Accession: T46070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199 NTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSG------EHNTVSGS-- 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : || || : || :| :|| || 248 HNRFSGAVPVSLCKHSLLEE---VSISHNQLSGSIPRECGGLPHLQSLDFSYNSINGTIP 304
                                      --DN 176
                                                                                                                                                                                                               -----NVVSGNDNNVSGSF--HTVSGEHN 241
                                                                                                                                                                                                                                                                                                                                                  IPKTICKLVSLDTLVLSNNNFNGSIPRCFEKFNTTLSVLHLRNNNLSGEFPEESISDHLR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable disease resistance protein [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T18N14.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 LLLCFLLFSAQAVAGGGGGGHSWDGIVVTQANYQALQAIKHELIDFTG-----VLKSWNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 MLLVFLGFILQV----AGATSW----SCHHDDLHALRGLAENLSGKGAVRLRAAWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 AS----CCSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 PKSLQIRLKSL-----TTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGT----
                                                                                                  186 GSAKLSGNFPSMLLNLSELTLIDLGSNOFGENOTTLYYLDISANKIGGOVPQWLWSLPEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   836;
                                      -NDSAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 184.5; DB 2; Length; Pred. No. 6.7e-06; 48; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule typeliminary
A;Residues: 1-836 <DEL>
A;Residues: 1-836 <DEL>
A;Cross-references: UNIPROT:Q9SCT4; EMBL:AL132968
A;Experimental source: cultivar Columbia; BAC clone T18N14
C;Genetics:
                                      SSRRTLDEEPNTISGIN--NSVGSGSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 625/1
A;Note: T18N14.120
C;Superfamily: protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 ----NNTVS---GSNHI 256
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                                                                                                                                                                                                                                                                                                           205 ----NHVVSGTKHIVTDNN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.3%;
illarity 25.7%;
Conservative 48
                                                                                                                                                                            TVVSGNNNHVSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                              TVSGSNNTVSG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLDVGRNRLSG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 82; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Accession: T46070
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R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2014
A.Title: Genome sequence of Yersinia pestis, the causative agent of plague. A; Reference number: AB0001; MUD:21470413; PMID:11586360
A, Reference number: AB0001; MUD:21470413; PMID:11586360
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-622 < KUR>
A, Residues: 1-622 < KUR>
A, Gross-references: UNIPROT:Q8ZGB5; GB:AL590842; PIDN:CAC99217.1; PID:g15979437; GSPDB:GCGenetics:
A, Gene: YP01388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LDLSGNSLVGEVPKSLQIRLKSLTTDSQ----SLGMG-----SINMLLHVSS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GNNNHVSGSNNTV 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 VTGSDNTVVGSNH----VVSGTKHIVTDNNNVVSGNDNNVSGSFHTVS-GEHNTVSGSNNT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 NNNGNGTINIFDASSNNDIHTLTGLGNEQ------LGGF-----SNHL-- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable disease resistance protein F18A5.210 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 24-Apr-1999 #sequence_revisi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLILSLSNSKLVLASHVKHLCRQDQKNALLEFKNEFYVHEFNSNGIVGVKKTEKWRNNTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GELDHLRYLDLSGNSLVGEVPKSLQIRLKSLTTDSQSL------GMGSINML--LHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CMLLVFLGF1LQVAGATSWSCHHDDLHALRGLAE-----NLSGKGAVRLRAAW-SGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.4%; Score 186; DB 2; Length 645;
22.1%; Pred. No. 3.8e-06;
ive 46; Mismatches 115; Indels 128; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---GLGGIIPSSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.7%; Score 190; DB 2; Length 62 Best Local Similarity 26.3%; Pred. No. 1.8e-06; Matches 68; Conservative 49; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T05251
R; Bevan, M.; Weber, N.; Grueninger, D.; Schmidheini, T.; Banc submitted to the Protein Sequence Database, February 1999
A; Reference number: Z15405
A; Accession: T05251
A; Molecule type: DNA
A; Residues: 1.645 < BVA
A; Residues: 1.645 < BVA
A; Residues: UNIPROT: 09SVNI; EMBL: AL035528
A; Experimental source: cultivar Columbia; BAC clone F18A5
C; Genetics:
A; Map position: 4
A; Introns: 216/1; 541/1
A; Note: F18A5.210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 RRT-LDEEPNTISGINNSVGSGSNNVVSGNDNTVVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCSWEGVGCETASGRVVALRL-----PKR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSGSNHI-VSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 22.1%
Matches 82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67
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GenCore version 5.1.6
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OM protein - protein search, using sw model

October 8, 2005, 02:09:36; Search time 41 Seconds (without alignments) 626.582 Million cell updates/sec Run on:

US-10-657-8528-15 1385 1 MPEYMAKCCMLLVFLGFILQ......NTVSGSNHIVSGSNKVVTDG 267 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description					probable disease r	probable disease r	probable protein k	hypothetical prote	hypothetical prote	probable disease r	probable receptor-	receptor kinase-li	hypothetical prote	probable receptor-	probable disease r	hypothetical prote	99.9K hypothetical	disease resistance	probable receptor-	hypothetical prote	protein kinase Xa2	cyst wall protein	76.4K protein kina	probable protein k	hypothetical prote	protein kinase hom	protein kinase TMK	Similar to disease	hypothetical prote
	ID	D84434	AF0169	T05251	T46070	G84524	C84633	B86440	AE1857	G96746	C96519	H84421	B85440	T05322	T00502	T00475	T47727	A86460	T17462	B84664	H86459	T10725	S61925	A86383	D96558	T49908	T05606	JQ1674	F86308	T10636
	DB	8	~	~	~	7	7	~	~	~	7	N	7	~	~	~	~	7	7	~	7	~	~	~	~	~	7	-	~	7
	Query Match Length	1008	622	645	836	983	743	590	420	1095	1019	716	166	1232	773	905	719	907	168	658	478	966	241	702	876	371	638	942	729	1143
%	Query	13.8	13.7	13.4	13.3	13.0	12.7	12.5	12.2	12.2	12.1		11.8	11.7	11.7	11.7	11.6	11.6	11.5	11.4	11.4	11.4	11.3	11.3	٠	•	•	11.2	•	11.2
	Score	190.5	190	186	184.5	179.5	176.5	173.5	169	168.5	168	164.5	164	162.5	162	161.5	191	191	159.5	158.5	158	157.5	157	156.5	156.5	156	156	155.5	155	154.5
;	Result No.	-	7	٣	4	'n	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote	probable disease r	probable receptor-	protein TIN15.9 (i	probable receptor	probable receptor-	probable disease r	probable protein k	hypothetical prote	receptor protein k	leucine-rich repea	probable receptor-	protein kinase Xa2	sericin MG-2 - gre	probable receptor	probable receptor-
T02361	T05257	B84852	G96524	A96557	H84632	T00971	F96557	F85343	T50851	T07079	B84782	T04313	C61615	E96631	B84659
~1	~	~	7	~	~	~	7	7	~	~	7	7	7	7	01
720	668	646	655	838	980	480	693	863	981	221	672	813	286	645	916
11.1	11.0	11.0	11.0	11.0	11.0	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8
154	153	152.5	152.5	152.5	152.5	151.5	151	151	151	150.5	150.5	150.5	149.5	149.5	149

ALIGNMENTS

RESULT 1

D84434	in accompany of the second of
C:Spec	plobate tereptorialisme procent Americana C:Species: Arabidoosis thaliana (mouse-ear cress)
C;Date	Cibite: 02-Peb-2001 #sequence revision 02-Feb-2001 #text_change 02-Feb-2001
C;Acce	C;Accession: D84434
R; Lin,	X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Ko	M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L
engs,	D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nacura A.T.+	Nature 402, 701-700, 137-700 Nature 402, 701-700, 137-700 A https://doi.org/10.000/10.000/10.000/10.000/10.000/10.000/10.000/10.000/10.000/
A:Refe	A. Reference number: A84420; MUID:20083487; PMID:10617197
A; Acce	A; Accession: D84434
A;Stat	A; Status: preliminary
A;Mole	A;Molecule type: DNA
A;Resi	A;Residues: 1-1008 <sto></sto>
A;Cros	A, Cross-references: GB: AE002093; NID: 96598459; PIDN: AAC78507.2; GSPDB: GN00139
C;Genetics:	Cjenetics: h.Game. h.Jan1220
A; Map	A.Yoric A.A.A. A.Yap position: 2
Š	
Quer	23.6%; SCOLE 190.3; DB 2;
Matc	best bocar Similarity 27.3%; Freu. NO. 3e-08; Matches 68; Conservative 45; Mismatches 93; Indels 41; Gaps 12;
δ	9 CMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW 64
qq	
ò	65 EGVGCET-ASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
i	
qq	66 TGITCNSNNTGRVIRLELGNKKLSGKLSESLGKLDEIRVLNLSRNFIKDSIPLSI-FNLK 124
δλ	124 SLTTDSQSLGMGSINMLLHVSSRRTLDEEPNTISGTNNSVGSGSNNV 170
qu	125 NLQTLDLSSNDLS-GGIPTSINLPALQSFDLSSNKFNGSLPSHICHNSTQIRVVKLAVNY 183
ò	171 VSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGN 225
á	S C COLUMNICATION TO THE STATE OF THE STATE
a	184 FAG

226 DNNVSGS 232 :|:||| 229 ENRLSGS 235

g ⋧ g AF0169
probable exported protein YP01388 [imported] - Yersinia pestis (strain CO92)
C.Species: Yersinia pestis
C.Space: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C.Accession: AF0169

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14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CE--TASGRVVALRIPKRGLGGIIPSSIGELDHIRYLDLSGNSLVGEVPKSL---QIRL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 KSLTTDSQSLGMGSI-NMLLHVSSRRTLDEEPNTISGTNNSVG------SGSNNVVSG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor off 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 MLLVFLGFILOVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAW-SGASCCSWEGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 NDNTVV---SGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 EIHPELCSSSGGIQVLDLSMNRLVGNLD----GLYNCSKSIQQLHIDSNRLTGQLPDYLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNK----VVTD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIRELEQUSLSGNY--LSGE---LSKNLSNLSGLKSLLISENRFSDVIPD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.7%; Score 258.5; DB 5; Length 1036; ilarity 30.7%; Pred. No. 1.6e-13; Conservative 50; Mismatches 98; Indels 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; SEQ ID NO 3015; 261pp + Sequence Listing; English
              Herbicidally active polypeptide SEQ ID NO 3015
                                                Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                       28-AUG-2001; 2001WO-EP009892.
                                                                                                                                                                                                                       28-AUG-2001; 2001WO-EP009892.
                                                                                  thaliana
                                                                                                                                                                                                                                                                                           Weidler
                                                                                                                                                                                                                                                                                                                           WPI; 2002-269010/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 89; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1036 AA;
                                                                                                                                                                                                                                                         (FARB ) BAYER AG.
                                                                                                                   WO200210210-A2.
                                                                                                                                                     07-FEB-2002
                                                                                                                                                                                                                                                                                           Tietjen K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Search completed: October 8, 2005, 02:16:38 Job time : 170 secs

(first entry)

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Anti-freeze protein; grass; plant; frozen food product; frost tolerance; frozen confectionery.
                                                                                                                                                                                                                                                                                                                                                                                New plant anti-freeze protein useful in frozen food products.
                                                      Grass anti-freeze protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 36; 39pp; English.
                                                                                                                                                                                                                                                                                                            Jarman CD, Sidebottom CM,
                                                                                                                                                                                                                                                                   (UNIL ) UNILEVER NV. (UNIL ) UNILEVER PLC
                                                                                                                                                                                                                                                                                                                                          WPI; 1999-458697/38.
                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX99717
                                                                                                                          Lolium perenne.
                                                                                                                                                       WO9937782-A2
                                                                                                                                                                                                             23-DEC-1998;
                                                                                                                                                                                                                                        22-JAN-1998;
                            29-SEP-1999
                                                                                                                                                                                   29-JUL-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
AAY22472;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB93804
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                                                                                                                                                                                                                                                                                         The present sequence is that of AFP1, an antificeeze protein of perennial ryegrass. The encoding cDNA was isolated from a pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall feecue) antificeaze proteins and the polynucleotides conciding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 LTTDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 NHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSPHTVSGEHNTV
                                                                                                                                                                                             reeze proteins and encoding polynucleotides, useful for og cold tolerance in organisms, as food additives, or for tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47.3%; Score 655; DB 8; Length 243; 51.9%; Pred. No. 1.8e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGS----NNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Mismatches
                                                                                                                             Hall C, Fish SA;
                                                                                                                                                                                                                                                                       Claim 7; SEQ ID NO 14; 71pp; English.
                                                                                  (GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHISON SEEDS LTD.
                                                        09-SEP-2002; 2002US-0409557P
                               09-SEP-2003; 2003WO-NZ000199
                                                                                                                                                                                                  New antifreeze proteins and modulating cold tolerance in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 51.9%
Matches 148; Conservative
                                                                                                                                                                                                                                              biocrystals (e.g. gout).
                                                                                                                             Demmer J, Shenk MA,
                                                                                                                                                          WPI; 2004-248453/23.
N-PSDB; ADM41458.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 243 AA;
  18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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Worrall

Twigg S,

98WO-EP008553. 98GB-00001408.

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This sequence is the plant anti-freeze protein of the invention. The anti-freeze protein is characterised in that at least 40% of its amino acids are from the group of serine, threonine and apparagine. The amino acids protein can be used in frozen food products, especially frozen confectionery. Anti-freeze proteins are especially in food products, which are heated, e.g. by pasteurisation, blanching or sterilisation prior to freezing. Plants transformed with a nucleic acid sequence encoding the auti-freeze proteins have an increased frost tolerance. Prior conforts freeze proteins have not been applied to commercially available frood products, due to high costs and complicated processes for obtaining the protein. Also prior art anti-freeze proteins have tended to commercially available confessions provide an ice particle size following an ice recrystallisation this is overcome by the present anti-freeze protein. The anti-freeze protein confining the pasteurisation step. This is overcome by the present anti-freeze protein ingreation indication as and the mixes can be frozen under quiescent conditions, e.g. in a shop or nome freezer without the formation of unacceptable ice crystal shapes and hears.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 DEEPNTISGINNSVGSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 GTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.3%; Score 530; DB 2; Length 11
85.5%; Pred. No. 7.3e-39;
ive 10; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB93804 standard; protein; 1036 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 100; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB93804;
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AAY22472 standard; protein; 118 AA.

RESULT 14 AAY22472 ID AAY2 XX σ

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Local Similarity
                                                                                                                                             frost or freezing.
                                                                                                                                                                Sequence 243 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lolium perenne.
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                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           107. .242
/note= "7-amino acid sequence repeat region identified in
                                     104
                                                62 NGASGRVITLWLPRRGLAGTITGASLAGLARLESLMLANNRLVGTIPSWIGELDHLLYLD 121
                                                                           163
                                                                                            LSHNSLVGELP-----NLKGLTTTGHLLGMAFTSMPLDVKPNRRTLAVQPNTISGTNNSV 176
                                                                                                               223
         -GIIPSSIGELDHLRYLD
                                                                          LSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGTNNSV
                                                                                                                GSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS
                                                                                                                          177 LSGRNYTVSGNDNTVISGNNNTVSGSFNTVVTGSDNVLTGSNHVVSGRNHIVTDNNNAVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is that of an antifreeze protein of tall fescue. encoding cDNA was isolated from a basal stem cDNA expression library. invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-

    64 / Anotes "Conserved Cys-pairs identified N-terminal Indian-rich repeats of receptor-like kinases"

                                                                                                                                                                                                                                                                                                    fescue; cold tolerance; transgenic; plant; antigout;
                                                                                                                                                      267
                                                                                                                                                                GDDNNVSGSFHKVSGSHNTVSGSNNTVSGRNHVVSGSNKVVTGG
                                                                                                                                                      GNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SA
                                                                                                                                                                                                                                                                                                                                                             1. .20
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                               nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; SEQ ID NO 15; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fish
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENESIS RES & DEV CORP LTD. WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                        ADM41472 standard; protein; 243
                                    ETASGRVVALRLPKRGLG----
                                                                                                                                                                                                                                                                                rall fescue antifreeze protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-SEP-2003; 2003WO-NZ000199
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                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-248453/23.
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                                                                                                                                                                                                                                                                                                                                Schedonorus
                                                                                                                                                                                                                                                                                                    Antifreeze;
                                                                                                                                                                                                                                                                                                              litholytic;
                                                                                                               164
                                                                                                                                                                                                                                            ADM41472;
                                    70
                                                                          105
                                                                                                                                                      224
                                                                                                                                                                                                                                                                                                                                                           Peptide
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different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to medulate the cold cold cannot be polynucleotides can be used to medulate the cold cold carded and bacteria. The method involves incorporating an antifreeze cold archaea and bacteria. The method involves incorporating an antifreeze cold cold cold cardenism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting coused for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NHVSGSNNTVVTGSDNTVVGSNHVVSGTKH1VTDNNNVVSGNDNNVSGSFHTVSGEH--- 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NVVSGSHNITVVFGGDNFLSGSNHVVSGNHHVVTDNKNAVSGDHNITVSGSQNTVSGNHHII 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "7-amino acid sequence repeat region identified in antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGNN 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLKS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTTAGRSLGKAFTNMPLHVKSSQGTLDEEHNTITGINNTVKSGSNNVVSGNDNTVISGNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAKCWQLLLFLAFLLPAASAA - - SRHPDDLRALQDFAGNLRGGGVV - LRAALSGGSCCDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----INTVSGSNNTVSGSNHIVSGSNKVVTDG
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53.0%; Pred. No. 1.2e-50;
ive 17; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ryegrass; cold tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antifreeze; perennial ryegrass; cold tolerance;
antigout; litholytic; nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGAGCDGASGRVT-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .20
/label= Signal_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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/note= "~
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New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                               perennial ryegrass; cold tolerance; transgenic; plant;
                                           antigout; litholytic; nephrotropic; cytostatic.
Perennial ryegrass antifreeze protein AFP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; SEQ ID NO 21; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-2002; 2002US-0409557P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Demmer J, Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2004-248453/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADM41465.
                                                                                                                                                                                                                                                                                                                                                                       WO2004022700-A2.
                                                                             Lolium perenne
                              Antifreeze;
                                                                                                                                                                                                                                                                                                                                                                                                        18-MAR-2004.
                                                                                                                            Peptide
                                                                                                                                                             Region
                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                             Region
                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                          Region
   The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) artifreeze proteins and the polymucleotides encoding them ADN41489.

ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the propersesion of an antifreeze protech can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. timour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 NGASGRITTLWLPRRGLACTITGASLAGLARLESLNLANNRLVGTIPSWIGELDHLLYLD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               164 GSGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVS 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSGNSLVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHVS-SRRTLDEEPNTISGTNNSV 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LILLFLGFLLPAACAATSSCHPDDLRALRGFAKNVGG-GGVLLRTAWSGTSCCVWEGVGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ------GIIPSSIGELDHLRYLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 LSGRANVVSGNDNTVISENNYTVSGSFNTVITGSDNVLTGSNHVVSGRSHIVTDNNNSVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 MLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSWEGVGC
                                                                                                                                                            New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 GNDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 65.1%; Score 901.5; DB 8; Best Local Similarity 65.5%; Pred. No. 3.5e-71; Matches 186; Conservative 17; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ETASGRVVALRLPKRGLG-------
                                                                                  Fish SA;
                                                                                                                                                                                                                                            Claim 7; SEQ ID NO 22; 71pp; English.
                               (GENE-) GENESIS RES & DEV CORP LTD (WRIG-) WRIGHTSON SEEDS LTD.
                                                                                  Hall C,
 09-SEP-2002; 2002US-0409557P.
                                                                                                                                                                                                                biocrystals (e.g. gout).
                                                                                  Demmer J, Shenk MA,
                                                                                                                WPI; 2004-248453/23
                                                                                                                                  N-PSDB; ADM41466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 285 AA;
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Fish SA;

Hall C,

'note= "7-amino acid sequence repeat region identified in

antifreeze proteins"

"Conserved lipoprotein membrane attachment site"

. .22 /label= Signal_peptide

location/Qualifiers

'note= "Conserved Cys-pairs identified N-terminal eucine-rich repeats of receptor-like kinases"

.63

note=

note= "Conserved leucine-rich repeats"

Transmembrane domain

.279

134. .153

note =

or

The present sequence is that of AFP4, an antifreeze protein of perennial regrass. The encoding cDNA was isolated from a leaf and pseudostem cDNA expression library. The invention provides forage grass (perennial regrass) and tall fescue) antifreeze proteins and the polynucleotides conciding them ADM41458-ADM41483. The plynucleotides were isolated from tissues taken at different times of year (winter and spring) and from confident parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded CRNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a control and be used to the organism, the state and the second as continged the disorder characterised by biocrystals associated with disorders such and the control as a control as the control as a control as an accordance and a control as a gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing. Gape 32; 63.8%; Score 884; DB 8; Length 280; 65.5%; Pred. No. 1.2e-69; ive 14; Mismatches 52; Indels Query Match 63.8° Best Local Similarity 65.5° Matches 186; Conservative Ź Sequence 280

ADM41478 standard; protein; 280 AA.

(first entry)

03-JUN-2004

ADM41478;

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110
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Peptide
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ADM41479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of AFP3, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a root cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, privace and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting
 224
                    237
                                                                                                                                                                                                                                                                                               .22
e= "Conserved lipoprotein membrane attachment site"
           SGNDNAVSGNDNTVICGNNNTVSGSNNTIASGSDNIVTGSNHIVCGTKHIITDNNNDVSG
SGSNINVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                           transgenic; plant;
                                                                                                                                                                                                                                                                                                                   53. 64
/note= "Conserved Cys-pairs identified N-terminal
leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                               "Conserved leucine-rich repeats"
                                            265
                                                      NDNNVSGSFHTVSGSHNTVSGSNNTVSGSNHVVSGSNKVVT 278
                                           NDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT
                                                                                                                                                                                                         ryegrass; cold tolerance; nephrotropic; cytostatic.
                                                                                                                                                                                    Perennial ryegrass antifreeze protein AFP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SA;
                                                                                                                                                                                                                                                                           1. .19
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; SEQ ID NO 18; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fish
                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                      AA.
                                                                                                                     ADM41475 standard; protein; 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP
(WRIG-) WRIGHTSON SEEDS LTD.
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                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gout).
                                                                                                                                                                                                                                                                                                                                                               /note= "
165. .27
/note= "
                                                                                                                                                                                                                                                                                                            'note=
                                                                                                                                                                                                          Antifreeze; perennial antigout; litholytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2004-248453/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 biocrystals (e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-248453/
N-PSDB; ADM41462.
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                    178
                                                              238
                                          225
                                                                                                                                            ADM41475;
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                                                                                                RESULT 9
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expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170. .284
/note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVGEVP----KSLQIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVG 164
                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                   MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGVGCDGTSGRVTALRIPISLEDCGKLKSLNLANERLVGTIPSWIGELDHHCYLVLSDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 SGSNNVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Conserved Cys-pairs identified N-terminal
leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fescue; cold tolerance; transgenic; plant; antigout;
                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                          Length 281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            238 NDNNVSGSFHTVSGSHNTVSGSNHVVSGSNKLVT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NDNNVSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265
                                                                                                                                                                                                                                                                        Score 901.5; DB 8;
Pred. No. 3.4e-71;
1; Mismatches 51;
                                                                                                                                                                                                                                                                                                                          21; Mismatches
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|Tabel= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADM41479 standard; protein; 285
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                                                                                                                                                                                                                                                                          65.1%;
66.2%;
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                                                                                                                                                                                                                                                                                                   Best Local Similarity 66.2
Matches 186; Conservative
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                frost or freezing.
                                                                                                                                                                                                                             Sequence 281 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004022700-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antifreeze;
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The present sequence is that of an antifreeze protein of perennial ryegrass and ryegrass. The invention provides forage grass (perennial ryegrass and tall feacue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold colorance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze opolymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by bhocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
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                                                    "Conserved lipoprotein membrane attachment site"
                                                                                                                                                                                                                                    /note= "7-amino acid sequence repeat region identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 EGVGCDGTSGRVTALRLPISLEDCGKLKSLNLANERLVGTIPSWIGELDHHCYLVLSDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                'note= "Conserved Cys-pairs identified N-termir
eucine-rich repeats of receptor-like kinases"
                                                                                                                                                                               /note= "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 65.3%; Score 904.5; DB 8; Best Local Similarity 66.5%; Pred. No. 1.8e-71; Matches 187; Conservative 20; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fish SA;
label= Signal_peptide
0. .22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 7; SEQ ID NO 26; 71pp; English.
                                                                                                                                                                                                                                                                  antifreeze proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GENE-) GENESIS RES & DEV CORP
(WRIG-) WRIGHTSON SEEDS LTD.
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                                                                                                                                                                                                           .279
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                                                      'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Demmer J, Shenk MA,
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N-PSDB; ADM41470.
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                                                                                                                                                                                                                                                                                                                      WO2004022700-A2.
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                                                                                                                                                                                                                                 The present sequence is that of an antifreeze protein of tall fescue. The invention provides forage grass (perennial ryegrass and tall fescue)

antifreeze proteins and the polynucleotides encoding them ADM41458-

ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of different times of year (winter and spring) and from different parts of che plants. The polynucleotides can be used to omodulate the cold cold archaea and bacteria. The method involves incorporating an antifreeze oplynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting consection of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 NAVSGNDNTVICGNNNTVSGSNNTIVSGSDNIVTGSNQVVCGTKHIITDNNNDVSGNDNN 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 LVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MAKCWLLLLFLVVLLPAASAT--SCHPDDLRALRGFVCNLNG-GGVLLHGAWSGSLCCAW
                                                      New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSGSSHTVSGSHNTVSGSNNTVSGSNHVVSGSNKVVT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 65.6%; Score 908.5; DB 8; Best Local Similarity 67.9%; Pred. No. 8e-72; Matches 188; Conservative 19; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perennial ryegrass antifreeze protein.
                                                                                                                                                                                        Claim 7; SEQ ID NO 19; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .19
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                                                                                                                                         biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lolium perenne.
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Key Peptide

THXSXMXXBXHX

ADM41483 RESULT

Gaps

23;

51; Indels

Length 281;

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Schedonorus arundinaceus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69. .124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-248453/23
                                      Sequence 277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004022700-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antifreeze;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        litholytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Demmer J,
                                                                                                                                                                 65
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                                                              Query Match
                                                                                                                                                                                                                                                                   169
                                                                                                                                                                                                                                                                                                                     229
                                                                                                                                                                                                                                                                                                                                                                                                                                    ADM41476;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is that of AFP3, an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41489. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals can be used for thick and kindney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a
                                                                                                                                                                                                                                                                                                                                                                     161. 275
/note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                 /note=""Conserved Cys pairs identified N-terminal of leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                   Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                        /note= "Conserved leucine-rich repeats"
             266
                        230 NTVSGSNNTVSGSNHVVSGSNKVVTD 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fish SA;
                                                                                                                                                                                                                                                                                1. .23
/label= Signal_peptide
                                                                                                                                                                             Perennial ryegrass antifreeze protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 7; SEQ ID NO 20; 71pp; English
                                                                                                                                                                                                                                                                                                                                                                                                antifreeze proteins"
           241 NTVSGSNNTVSGSNHIVSGSNKVVTD
                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                  ADM41477 standard; protein; 277 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-SEP-2003; 2003WO-NZ000199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-2002; 2002US-0409557P
                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                               69. .125
                                                                                                                                                                                                                                                                                                          . 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treating tumors or disobiocrystals (e.g. gout)
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                                                                                                                                                                                                                                         Lolium perenne
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                                                                                                                           ADM41477;
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/note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                                                                                                                                  EGVGCETASGRVVALRLP------KRGLGGIIPSSIGELDHLRYLDLSGNS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVGEVPKSLQIRLKSLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 EGVGCDGTSGRVTALRLPISLEDCGKLKSLNLANERLVGTIPSWIGELDHHCYFVLSDNS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 NAVSGNDNTVMCGNNNTVSGSNNTISSGSDNIVTGSNHIVCGTKHIITDNNNDVSGNDNN 237
                                                                                                                                                                                                                                                       5 MAKCCMLLVFLGFILQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCSW 64
                                                                                                                                                                                                                                                                                       1 MAKCWLILLEFLVFILLAVCAT--SCHPDDLRALRGFVGNING-GGVILRETWSGSSCCAW 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Conserved lipoprotein membrane attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NVVSGNDNTVVSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNNVVSGNDNN
patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.
                                                                                                                                                                                                    Gaps
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/note= "Conserved Cys-pairs identified N-terminal
leucine-rich repeats of receptor-like kinases"
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                                                                                                                                                                                                 19;
                                                                                                                                          Length 277;
                                                                                                                                          65.7%; Score 910.5; DB 8; Length 2
67.5%; Pred. No. 5.3e-72;
ive 20; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 VSGSFHTVSGSHNTVSGSNNTVSGSNHVVSGSNKVVT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSGSFHTVSGEHNTVSGSNNTVSGSNHIVSGSNKVVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .22
/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fescue; cold tolerance; t nephrotropic; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADM41476 standard; protein; 277 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tall fescue antifreeze protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-SEP-2003; 2003WO-NZ000199
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                                                                                                                                                                    Best Local Similarity 67.59
Matches 187; Conservative
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                                                                         The present sequence is that of AFP5, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze plypeptide. The autifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect. a plant from damage due to frost or freezing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 WEGVGCDGASGRVTALMLPRSGLTGP1PSW1CQLHHLRYLDLSGNALVGEVPRNLQVQLK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         229
                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAKCLMLLLSFAFLLSVAGTATATPCHRDDLRALRGFAENLGGGGAISLRAAWSGASCCD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 MAKCCMLLVFLGFILQVAG-ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 SLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNT
as food additives, or for with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antifreeze; perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
                                                                                                                                                                                                                                                                                                                                                                                                          Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                       70.8%; Score 980.5; DB 8; 73.5%; Pred. No. 3e-78; ive 24; Mismatches 33;
  modulating cold tolerance in organisms, treating tumors or disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .23
/label= Signal_peptide
59. .70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perennial ryegrass antifreeze protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSGSNNTVSGSNHIVSGSNKVVTD 266
                                                         Claim 7; SEQ ID NO 23; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM41482 standard; protein; 256 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 73.5
Matches 194; Conservative
                              biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                                                                              Sequence 254 AA;
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Region

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The present sequence is that of an antifreeze protein of perennial ryegrass. The encoding CDNA was isolated from a leaf and pseudostem CDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polyuncleotides (perennial rissues taken at different times of year (winter and spring) and from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polyuncleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polyuncleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polyuncleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypoptide. The autifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 CSWEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence repeat region identified in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to frost or freezing.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 GININHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 MAKCCMLLVFLGFILQVAG---ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
      ö
note= "Conserved Cys-pairs identified N-terminal eucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34; Indels
                                                                                                  "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 973.5; DB 8;
Pred. No. 1.3e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fish SA;
                                                                                                                                                                   /note= "7-amino acid
antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; SEQ ID NO 25; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hall C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-SEP-2002; 2002US-0409557P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biocrystals (e.g. gout)
                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Demmer J, Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2004-248453/23
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                                                                                                                                                                                                                                                                      WO2004022700-A2
                                                                                                                                                                                                                                                                                                                                       18-MAR-2004.
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                                                                                                                                        Region
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The present sequence is that of an antifreeze protein of tall fescue. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them ADM41458-
ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolarance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide, in a method for decreasing the time required to a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrysteals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147. .261
/note= "7-amino acid sequence repeat region identified in
antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                     57. .68 — Conserved Cys-pairs identified N-terminal leucine-rich repeats of receptor-like kinases"
                                                                                                                                                                                                                                                                 fescue, cold tolerance, transgenic, plant, antigout, nephrotropic, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73. .114
/note= "Conserved leucine-rich repeats"
241 EHNTVSGSNNTVSGSNHVVSGSNKVVTDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                  1. .23
/label= Signal_peptide
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                                                                                                               ADM41481 standard; protein; 262
                                                                                                                                                                                                                            Tall fescue antifreeze protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-2003; 2003WO-NZ000199
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                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                         Schedonorus arundinaceus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biocrystals (e.g. gout)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2004022700-A2
                                                                                                                                                                                         03-JUN-2004
                                                                                                                                                                                                                                                               Antifreeze;
litholytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2004
                                                                                                                                                    ADM41481;
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                                                                                                                                                        64 WEGVGCETASGRVVALRLPKRGLGGIIPSSIGELDHLRYLDLSGNSLVGEVPKSLQIRLK 123
                                                                                                                                                                                           124 SLTTDSQSLGMGSINMLLHV-SSRRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTVVSGN 182
                                                                                                                                                                                                       NNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSGEHNT 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "7-amino acid sequence repeat region identified in
                                                                                                                                                                                                                                                       NNSVSGSNNTVVSGSDNTVTGSNHVVSGTNHIVTDNNNNVSGNDNNVSGSFHTVSGGHNT 237
                                                                                                                   9
                                                                                                           1 MAKCLMILLISFAFILSAAGTATATPCHRDDLRALRGFAENLGGGGALSLRAAWSGASCCD
                                                                                             MAKCCMLLVFLGF1LQVAG-ATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGASCCS
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifreeze, perennial ryegrass; cold tolerance, transgenic; plant, antigout; litholytic; nephrotropic, cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57. .68
/note= "Conserved Cys-pairs identified N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antifreeze proteins and encoding polynucleotides, useful for
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Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             leucine-rich repeats of receptor-like kinases"
                                              Length 262;
                                    71.7%; Score 992.5; DB 8; Lengua. 75.0%; Pred. No. 2.8e-79; Ladels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Conserved leucine-rich repeats"
139. .253
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perennial ryegrass antifreeze protein AFP5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .23
/label= Signal_peptide
                                                                                                                                                                                                                                                                                           VSGSNNTVSGSNHIVSGSNKVVTD 266
                                                                                                                                                                                                                                                                                                       VSGSNNTVSGSNHVVSGSNKVVTD 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antifreeze proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                            ADM41480 standard; protein; 254 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hall C,
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                                             Query Match
Best Local Similarity 75.0
Matches 198; Conservative
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frost or freezing
                       Sequence 262 AA;
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Misc-difference 124
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                The present sequence is that of AFP2, an antifreeze protein of perennial ryegrass. The encoding cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and thal fescue) antifreeze proteins and the polynucleotides conciding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from clifferent parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopresservation of a cell or cissue, as a food additive of a frozen food product, in a method for descreasing the time required to dehydrate a composition, to treat a confiscent characterised by biocrygtals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and contect a plant from damage due to frost or freezing.
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                 Length 267;
                                                                                                                                                                                                                                                                                                                                                          Indels
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/note= "Conserved leucine-rich repeats"
                                                                                                                                                                                                                                                                                                                               100.0%; Score 1385; DB 8;
ilarity 100.0%; Pred. No. 5.4e-114;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NTVSGSNNTVSGSNHIVSGSNKVVTDG 267
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/label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nephrotropic; cytostatic.
 Claim 7; SEQ ID NO 16; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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Matches 267; Conserv
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Peptide
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154. .268
/note= "7-amino acid sequence repeat region identified in
antifreeze proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 IRLKSLTTDSQSLGMGSINMLLHVSS-RRTLDEEPNTISGTNNSVGSGSNNVVSGNDNTV 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       179 VSGNNNHVSGSNNTVVTGSDNTVVGSNHVVSGTKHIVTDNNNVVSGNDNNVSGSFHTVSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MPEYMAKCCMLLVFLGFI-LQVAGATSWSCHHDDLHALRGLAENLSGKGAVRLRAAWSGA
                                                                                                                                                                                                                                                                                                                          New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1290; DB 8;
Pred. No. 1.4e-105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.1%; Scc...
93.3%; Pred. No. 1....
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    239 EHNTVSGSNNTVSGSNHIVSGSNKVVTDG 267
                                                                                                                                                                                                                                                   SA;
'note= "Encoded by TAG'
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; SEQ ID NO 17; 71pp; English.
                                                                                                                                                                                                                                                   Fish
                                                                                                                                                                                                                                                   Demmer J, Shenk MA, Hall C,
                                                                                                                                         09-SEP-2003; 2003WO-NZ000199.
                                                                                                                                                                      09-SEP-2002; 2002US-0409557P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 93.3
Matches 251; Conservative
                                                                                                                                                                                                                                                                                                                                                                              biocrystals (e.g. gout).
                                                                                                                                                                                                    (GENE-) GENESIS RES & DE
(WRIG-) WRIGHTSON SEEDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or freezing
                                                                                                                                                                                                                                                                                                  N-PSDB; ADM41461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 269 AA;
                                                                             WO2004022700-A2
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Pinus rad Herbicida

Protein e

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Aab25515 Aaw68208

catarr

Pinus rad Pinus rad Pinus rad

Aab25518 Abb91206 Aab25445 Aab25527 Aab25512 Aaw68204

M. catarr Pinus rad Herbicida Cell prol Rice stre Herbicida Thale cre Soybean r

Aab25413 Abb91562 Adq36979 Adq15649 Abb91915 Adi32622 Aam42230 Aam42230 Aam42230 Abb992188 Abb992188

Soybean r Soybean r Herbicida

Thale cre

OM protein

е 6

Sequence:

Searched:

Database

Result No.

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/note=""Conserved leucine-rich repeats"
152. .266
/note= "7-amino acid sequence repeat region identified in
antifreeze proteins"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic.

    71
    /note= "Conserved Cys pairs identified N-terminal
leucine-rich repeats of receptor-like kinases"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perennial ryegrass antifreeze protein AFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    ALIGNMENTS
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/label= Signal_peptide
                  AAW68208
AAW68208
ABB91206
AAB25445
AAB25445
AAB255412
AAB255112
AAW68204
AAW625113
ABB91562
ADQ36979
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AAW42230
AAM42230
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AAM42232
AAM42232
AAM42232
AAM42232
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(WRIG-) WRIGHTSON SEEDS LTD.
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N-PSDB; ADM41460.
WO2004022700-A2
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                    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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104 GCAACGTCGTGGTCGTGCCACCACGACCTCCACGCGTTGAGGGGCCTCGCTGAGAAC 163
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ne : 767 secs
PRIOR APPLICATION NUMBER: US 60/325,277
.PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO 1496
LENGTH: 4536
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Best Local Similarity 63.11
Matches 157; Conservative
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; LOCATION: (661)..(661)
; OTHER INFORMATION: n =
US-10-260-238-1496
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Sequence 1496, Application US/10260238

Publication No. US20040016025A1

SEQUENCE INTERPORMATION:

APPLICANT: Budworth, Paul R.

APPLICANT: Briggs, Steven P.

APPLICANT: Cooper, Bret

APPLICANT: Goff, Stephen A.

APPLICANT: Katagiri, Fumiyaki

APPLICANT: Kreps, Joel

APPLICANT: Kreps, Joel

APPLICANT: Ricke, Darrell

APPLICANT: Zhu, Tong

TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION

TITLE OF INVENTION NUMBER: US/10/260,238

CURRENT APPLICATION NUMBER: US/20/266,238

CURRENT FILING DATE: 2002-09-26

PRIOR PPLICATION NUMBER: US 60/325,448
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US-10-437-963-77805
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LOCATION: (1)..(3285)
OTHER INFORMATION: unsure at all n locations
                             La Rosa, Thomas J.
Kovalic, David K.
Zhou, Yihua
Cao, Yongwei
Wu, Wei
Baukharov, Andrey A.
Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            341 TTGGATCTC 349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 77805
LENGTH: 3285
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       652 GTATCCGGGAACCACCATATCATATCTGCGAGCCACAGTACCATATCCGGGAACCACAAT 711
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                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
    APPLICANT: Denmer, Jercen
; APPLICANT: Benk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
; TITLE OF INVENTION: Grasses and methods for their use.
; TITLE OF INVENTION: MUMBER: 2003-09-09
; FILE REFERENCE: 11000-1070U
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR APPLICATION NUMBER: 60/409,557
; PRIOR PRING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FRAUSEQ for Windows Version 4.0
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787 AGCTTCCATAAAGTATCTGGAAGTCACAATACGGTATCTGGGAGCAACAATACCGTATCC
                                                                         GGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAATATTCTGTA
                                                                                                                        848 GGTGCA-------GGATTGCTTCCATCTTCCCAAGTTCAGTGTAGCT
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PUblication No. US20040146884A1
GENERAL INFORMATION:
APPLICANT: Demmer, Jeroen
APPLICANT: Benk, Michael Andrew
APPLICANT: Hish, Steven A
TITLE OF INVENTION: Artifreeze proteins isolated from forage
TITLE OF INVENTION: Artifreeze proteins isolated from forage
TITLE OF INVENTION: Artifreeze proteins isolated from forage
TITLE OF INVENTION: 2003-09-09
FILE REFERENCE: 11000.1070U
CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT FILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.1e-77;
0; Mismatches 116;
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Best Local Similarity 74.8%;
Matches 353; Conservative (
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ORGANISM: Festuca arundinacea
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Query Match

Best Local Similarity 67.2%;
Matches 711; Conservative (
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; ORGANISM: Pestuca arundinacea
US-10-657-852-8
                                                              LENGTH: 1064
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; Sequence 8, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
; APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
; APPLICANT: Hall, Claire
; APPLICANT: Fish, Steven A
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Db 456 GACTCAAGGCCTCGCTGGTTCACTAGGTATGCTTTCGCTAACATGCCAT 515 Qy 456 TGCATGTGAGCAGTAGAAGACCTCGATGAAACAATACAAT	Qy 633 CTGTAGTTGGTAGCAACGATGTGTGTATCGGGACAAAGCATATGTTACTGATAACAATA 696 Db 696 TCGTAACTGGCAACCATATTGTATGTGGGACCAAACATATCATAACTGATAACAACA 755 Qy 693 ATGTTGTATCGGGAACAATAATGTGTCTGGAAGCTTCCATACTGATCAGGGAGC 756 ATGACGTATCCGGAACAATAATGTCTTGGAAGCTTCCATACTGTATCGGGAGC 815 ACAATACCGTATCCGGAACAATAATGTATCTGGGAACAACATGTTCTGGGAGCAACCATGTTCTGGGAGCAACATGTTCTGGAACAACAACACATGTTCTGGAACAACAACAACAACAACAACAATGTTTGTAAGAACAACAATGTTCTGGAACAATCTTGGAACAATCTTGGAACAACAACAATATTGTAAGAACAAACA	RESULT 10 US-10-657-852-5 ; Sequence 5, Application US/10657852 ; Publication No. USZ0040146884A1 ; GENERAL INFORMATION: ; APPLICANT: Demmer, Jeroen ; APPLICANT: Shenk, Michael Andrew ; APPLICANT: Fish, Steven A ; TITLE OF INVENTION: Attifreeze proteins isolated from forage ; TITLE OF INVENTION: Agrasses and methods for their use. ; TITLE OF INVENTION: Agrasses and methods for their use. ; TITLE OF INVENTION UNBER: US/10/657,852 ; CURRENT FILING DATE: 2002-09-09 ; RILIS REPERENCE: 11000.107001 ; CURRENT APPLICATION NUMBER: 60/409,557 ; PRIOR PILING DATE: 2002-09-09 ; NUMBER: OF SEQ ID NOS: 44 ; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 5 ; LENGTH: 1084 ; TYPE: DNA ; ORGANISM: Festuca arundinacea US-10-657-852-5	Query Match 42.6%; Score 417.4; DB 22; Length 1084; Best Local Similarity 70.3%; Pred. No. 4e-126; Actober 701; Gaps 7; Qy 33 CCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGGTGTTCTTTGGGGTTCATCTTGC 92
	VS-10-657-852-13 US-10-657-852-13 Sequence 13, Application US/10657852 Publication No. US20040146884A1 GENERAL INFORMATION: APPLICANT: Demmer, Jeroen APPLICANT: Shenk, Michael Andrew APPLICANT: Hall, Claire APPLICANT: Fish, Steven A TITLE OF INVENTION: Grases and methods for their use. TITLE OF INVENTION: Grases and methods for their use. TITLE OF INVENTION: Grases and methods for their use. CURRENT APPLICATION NUMBER: US/10/657, 852 CURRENT APPLICATION NUMBER: 60/409, 557 PRIOR APPLICATION NUMBER: 60/409, 557 NUMBER OF SEQ ID NOS: 44 SSOPTHARE: FastSEQ for Windows Version 4.0 SSOPTHARE: PastSEQ for Windows Version 4.0 SSOPTHARE: PastSEQ for Windows Version 4.0 STATES DATE: US ORGANISM: Lolium perenne US-10-657-852-13	Query Match 42.8%; Score 419; DB 22; Length 1083; Best Local Similarity 70.4%; Pred. No. 1.2e-126; Matches 702; Conservative 0; Mismatches 205; Indels 90; Gaps 7; Qy 33 CCATGCCTGAATACATGGCAAAGTGTTGCTGCTGCTGCTTTTTTGGGTTCTTTTGGTTGTTTTTGGTTGTT	Oy 288 GCCTTGGAGGATCATCCCATCGTCGATTGTGACCTTGATCACCTTTGGATC 347

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Sequence 9, Application US/10657852
Publication No. US20040146884A1
GENERAL INFORMATION ...
APPLICANT: Demmer. Michael Andrew
APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire

RESULT 8 US-10-657-852-9

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                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                             Length 1246;
                                                                                                                                                                                                                                                                             Indels 103;
APPLICANT: Fish, Steven A TITLE OF INVENTION: Attifreeze proteins isolated from forage TITLE OF INVENTION: Attifreeze proteins isolated from forage TITLE OF INVENTION: grasses and methods for their use. FILE REPERBYCE: 11000.1070U CURRENT APPLICATION NUMBER: US/10/657,852 CURRENT FILING DATE: 2003-09-09 PRIOR APPLICATION NUMBER: 60/409,557 PRIOR FILING DATE: 2002-09-09 NUMBER OF SEQ ID NOS: 44 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 9: LENGTH: 1246
                                                                                                                                                                                                                                              Score 421.8; DB 22;
Pred. No. 1.5e-127;
0; Mismatches 192;
                                                                                                                                                                                                                                              43.0%;
llarity 70.1%;
Conservative (
                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Festuca arundinacea
US-10-657-852-9
                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                               690;
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Best Local S
Matches 690
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953 CCTTGTCCAAGTTCAGTGTAGCTCACAGTCACTGGTAGGGACAATCGAGTTATGTAACT 1012
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                                                                                                                      GCAGTAGAAGAACGCTCGATGAAGAACCAAATACAATATCAGGGACCAACAATAGTGTTG
   TCACCACTGACAGCCAGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGTGA---
                                                                                                                                                                                                                                                                                                                                                           585 ACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10657852; Publication No. US20040146884A1; General Information No. US20040146884A1; General Information:

APPLICANT: Demmer, Jeroen

APPLICANT: Shenk, Michael Andrew

APPLICANT: Hall, Claire

APPLICANT: Hish, Stewen A

ITLE OF INVENTION: Antifreeze proteins isolated from forage

ITLE OF INVENTION: Grasses and methods for their use.

FILE REFERENCE: 11000.1070U

CURRENT PRILING DATE: 2003-09-09

PRIOR APPLICATION NUMBER: 60/409,557

PRIOR FILING DATE: 2002-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Pred. No. 9.8e-135;
0; Mismatches 209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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Best Local Similarity 71.2%;
Matches 706; Conservative
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US-10-657-852-7
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                               --CCCAAGTTCAG
                                                                                                                                                                                                                                        TGTAGCTTACAATCAATAGATGGAGACAATCACGTTATGTAACTTCA-GGATATGGCATA
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CTGTATCCGGGAGCAACCATATCGTGAGCAACAAAGTCGTAACAGATGGTTAAT
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46.0%; Score 451.2; DB 22; Length 1230;
Best Local Similarity 72.0%; Pred. No. 3.1e-137;
Matches 708; Conservative 0; Mismatches 198; Indels 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/10657852

Publication No. US20040146884A1

GENERAL INFORMATION:

APPLICANT: Demmer, Jercen

APPLICANT: Shenk, Michael Andrew

APPLICANT: Hish, Steven

TITLE OF INVENTION: Antifreeze proteins isolated from forage

TITLE OF INVENTION: Antifreeze proteins isolated from forage

TITLE OF INVENTION: UNGRER: 1000.1070U

CURRENT APPLICATION NUMBER: 1050.1070U

CURRENT APPLICATION NUMBER: 60/409.557

PRIOR APPLICATION NUMBER: 60/409,557

PRIOR APPLICATION STATE: 2002-09-09

WHORE TILING DATE: 2002-09-09

NUMBER: 6080 ID NOS: 44

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                           CTTTTC---CTTTAAATAAAGCTTCCCTTTACATAAAAAAA 980
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LENGTH: 1230
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164 ATGACCTTCGCGCGCTGCGGGCTTCGCTGAGAACCTGGGCGGCGGCGGCGCATCAGCC
                                                       CCAGCGGCCGTGTCACGGCTTTGTGGCTCCCCAGGAGCGGCCTCACGGGCCAATCCCGT
                                                                                                              CTGGGAGCAACCACGTTGTATCTGGAAGCAACAAAGTCGTGACAGACGCTTAATGATCTG
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Sequence 12, Application US/10657852 Publication No. US20040146884A1 GENERAL INFORMATION: APPLICANT: Demmer, Jeroen APPLICANT: Shenk, Michael Andrew

US-10-657-852-12

719 396 599 629 422 AGTCACTCGGTATGGGTTCCATTAACATGCTATTGCATGTGA---GCAGTAGAAGAACGC 479 539 603 663 122 156 ACCACGACCACCACCACGCGTTGAGGGCCTCGCTGAGAACCTAAGCGGCAAAGGAGCCG 182 276 483 96 71 TGGTTGGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCC CAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATG TCTTCTTGGGGTTCATCTTGCAGGTGGCAGGA-----GCAACGTCGTGGTCGTGCC 157 ACCGCGATGACCTTCGCCCGCGCTGCGGGGCTTCGCTGAGAACCTGGGCGGCGGCGGCGCGCCCAC Acecreteckédedetetrévedetriverederedekédededetrekedededetra TCGATGAAGAACCAAATACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACA ATGITGITTCCGGGAATGACACACGGTCGTATCTGGGAATAACAACCATGTGTCTGGGA GCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT GCAACAACACTGTCGTAAGTGGGGAATGACAATACCGTAACCGGCAGCAACCATGTCGTAT restrigeceagetacceaagaarcrecaegracaecreaaagecareacc-----AATCAAGGTTTCTTGTTCAATCCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGG TCCGCCTCCGCGCCCTCCGGCCCTCATGCTGCAGCTGGGAAGGTGTGGGATGCG TCCCATCGTCGATTGGTGATCACCTTCGCTATTTGGATCTCGGGTAATTCAT Gaps 68; Length 1007; forage Query Match
50.3%; Score 492.8; DB 22; Length
Best Local Similarity 73.6%; Pred. No. 5.1e-151;
Matches 739; Conservative 0; Mismatches 197; Indels APPLICANT: Hall, Claire
APPLICANT: Fish, Steven A
TITLE OF INVENTION: Antifreeze proteins isolated from fora
TITLE OF INVENTION: Antifreeze proteins isolated from fora
TITLE OF INVENTION: JASSES and methods for their use.
FILE REFERENCE: 11000.1070U
CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/409,557
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 1007 099 664 720 724 ò g à g m

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439 TITCACCAACATGCCATTGCATGTGATGCGTAACAGAAGATCACTCGACGACGAGCAGCCCAA 498
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                                                                  499 TACAATATCTGGGAGCAACAACAATACTGTCAGATCCGGGAGCAAAAATGTTGCTGGGAA
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Sequence 10, Application US/10657852

Publication No. US20040146884A1

SERNERAL INFORMATION:

APPLICANT: Demmer, Jercen

APPLICANT: Fish, Michael Andrew

APPLICANT: Fish, Steven A

TITLE OF INVENTION: Antifreeze proteins isolated from forage

TITLE OF INVENTION: Antifreeze proteins for their use.

FILE REFERENCE: 11000.1070U

CURRENT FILING DATE: 2003-09-09

FRIOR APPLICATION NUMBER: 60/409.557

FRIOR APPLICATION NUMBER: 60/409.557

FRIOR PILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 44

SOFTWARE: FESTERE for Windows Version 4.0
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CAACACTGTATCCGGGGGGGAACCATGTCGTATCTGGAAGCAACAAAGTCGTAACAGATGG
                                                                                                                   AATAGATGGAGACAATCACGTTATGTAACTTCAGGATATGGCATACTTTTCCTTTAAATA
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                                                TTAATATTCTGTAGGTGCAGGATTGCTTCCATCTTCCCAAGTTCAGTGTAGCTTACAATC
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Bublication No. US20040146884A1

GENERAL INFORMATION:

APPLICANT: Demmer, Jercen

APPLICANT: Bennk, Michael Andrew

APPLICANT: Hish, Steven A

TITLE OF INVENTION: Antifreeze proteins isolated from forage

TITLE OF INVENTION: Antifreeze proteins isolated from forage

TITLE OF INVENTION: Grasses and methods for their use.

FILE REFERENCE: 11000.10700

CURRENT APPLICATION NUMBER: US/10/657,852

CURRENT FILING DATE: 2003-09-09

PRIOR PILING DATE: 2002-09-09

PRIOR FILING DATE: 2002-09-09

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PastSEQ for Windows Version 4.0

LENGTH: 1006
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                                                                                                                                                                                                           ORGANISM: Festuca arundinacea
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Matches 756; Conservative
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APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire
APPLICANT: Fish, Steven A
TITLE OF INVENTION: Antifreeze proteins isolated from fora;
TITLE OF INVENTION: Antifreeze proteins isolated from fora;
TITLE OF INVENTION: Grasses and methods for their use.
FILE REPERENCE: 11000.1070U
CURRENT APPLICATION NUMBER: US/10/657,852
CURRENT FILING DATE: 2003-09-09
PRIOR FILING DATE: 2002-09-09
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                 Indels
                                                                                                                                                                                           DB 22;
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                                                                                                                                                                                           Score 904.4; DB 22
Pred. No. 8.6e-287;
0; Mismatches 31;
                                                                                                                                                                                             92.3%;
                                                                                                                                            ; TYPE: DNA
; ORGANISM: Festuca arundinacea
US-10-657-852-4
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Sequence 4, Application US/10657852 Publication No. US20040146884A1 GENERAL INFORMATION: APPLICANT: Demmer, Jeroen

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13: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/USO0P_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/U
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                        - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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980
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Sequence 6767, Ap
Sequence 7515, Ap
Sequence 138064,
Sequence 105088,
Sequence 24982, A
Sequence 39626, A
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Sequence 30, Appl
Sequence 30, Appl
Sequence 4582, Ap
Sequence 4584, Ap
Sequence 47843, A
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Sequence 17805, A
Sequence 1496, Ap
Sequence 12, Appl
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Sequence 102064,
Sequence 102066,
Sequence 107066,
Sequence 861, App
Sequence 861, App
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; Sequence 3, Application US/10657852
; Publication No. US20040146884A1
; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Demmer, Jeroen
; APPLICANT: Shenk, Michael Andrew
APPLICANT: Hall, Claire
; APPLICANT: Hall, Claire
; APPLICANT: Hall, Claire
; TITLE OF INVENTION: Antifreeze proteins isolated from forage
TITLE OF INVENTION: Grasses and methods for their use.
FILE REFERENCE: 11000.1070U
; CURRENT APPLICATION NUMBER: US/10/657,852
; CURRENT APPLICATION NUMBER: 60/409,557
; PRIOR APPLICATION NUMBER: 60/409,557
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 3:
LENGTH: 980
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US-10-657-852-9

US-10-657-852-13

US-10-657-852-8

US-10-657-852-8

US-10-657-852-1

US-10-657-852-1

US-10-657-852-1

US-10-657-852-1

US-10-37-082-12

US-10-765-790-12

US-10-77-790-12

US-10-77-790-12

US-10-77-790-12

US-10-765-790-12

US-10-765-790-12

US-10-765-790-12

US-10-260-238-568

US-10-027-632-102065

US-10-037-933-7358

US-10-101-464A-861

US-10-437-963-7555

US-10-425-115-155868

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US-10-425-115-105088

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US-10-425-115-105088
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Sequence 11, Sequence 10, Sequence 12,

US-10-657-852-3 US-10-657-852-4 US-10-657-852-11 US-10-657-852-12 US-10-657-852-12 US-10-657-852-6 US-10-657-852-6

996 1006 1008 1230

904.4 541.6 503.6 492.8 451.2

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Sequence Sequence

Sequence 3,

Sequence

Description

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Length

Query Match 1

Score

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604 CAACACTGTTGTAACTGGA 622 ::: || :| :| :| 43 425 YMWTTCTCWTWTWYGTTRA 443

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Search completed: October 8, 2005, 20:02:20 Job time : 215 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTGGGGAGGTACCAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCA 423
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Pred. No. 0.081;
0; Mismatches 83; Indels
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APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 05.4FR2;
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 15639
LENGTH: 505
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SUTYARRE: PastSEQ for Windows Version 4.0
SEQ ID NO 421
LENGTH: 498
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ilarity 51.5%;
Conservative 0
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Best Local Similarity
Matches 88; Conserv
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US-09-621-976-15639
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US-10-101-464A-421
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| GENERAL INFORMATION:
| JAPPLICANT: Strabala, Timothy
| APPLICANT: Nieuwenhuizen, Nicolaas
| APPLICANT: Higgins, Colleen M. |
| TITLE OF INVENTION: Compositions Isolated from Plant Cells |
| TITLE OF INVENTION: Compositions Isolated from Plant Cells |
| TITLE OF INVENTION: Compositions Isolated from Plant Cell Signaling |
| FILE REFREENCE: 11000.1020c2 |
| FILE REFREENCE: 11000.1020c2 |
| FILE REFREENCE: 1000.0020c2 |
| FRIOR PRICATION NUMBER: 09/704,302 |
| PRIOR FILING DATE: 2000-11-01 |
| PRIOR FILING DATE: 1990-01-12 |
| PRIOR FILING DATE: 1990-11-01 |
| PRIOR FILING DATE: 1990-11-01
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GENERAL INVENTATION:

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Higgins, Collean M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020.2

FILE REFERENCE: 1000.1020.2

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2000-11-01

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR PILING DATE: 1999-01-12

PRIOR PILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR PILING DATE: 1999-11-01

PRIOR APPLICATION NUMBER: PCT/US00/00724
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      297 CCCTGAGTGCTGGTTGAATGGTACGCTCTCCCCGTATATTGGGAACCTCTCTTTTTGCG 356
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                                                                   337 CTATTTGGATCTCTCGGGTAATTCATTGGTTGGGGAGGTACCAAAAAGTTT 387
                                                                                                                                357 GCATTTAGATCTTTGGAATGCTTTGAGTGGGAGAATTCCAGCAGAGTT 407
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Pred. No. 0.077;
0; Mismatches 83; Indels
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APPLICANT: Strabala, Timothy
                                                                                                                                                                                                                                                                                               Sequence 39, Application US/10101464A Patent No. 6768041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 51.5%;
Matches 88; Conservative
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US-10-101-464A-421
                                                                                                                                                                                                                              RESULT 13
US-10-101-464A-39
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Sequence 39, Application US/09228986
Fatent No. 6359198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION OPER: 1399-01-12
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAACAGCAAGCGGCCGCCGTCGTGGCGTTGCGGCTCCCCAAGCGCGCCTTGGAGGGATCA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGTAATTCAT 362
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3.9%; Score 38.4; DB 4; Length 2
Best Local Similarity 49.6%; Pred. No. 0.21;
Matches 127; Conservative 0; Mismatches 126; Indels
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CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 05/162,866
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR PLING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FESTSEQ for Windows Version 4.0
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Matches 88; Conservative
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US-09-228-986-39
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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 1100.0.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
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Patent No. 6768041
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL HOSPITION:
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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3.9%; Score 38.4; DB 4; Length 1107;
Best Local Similarity 49.6%; Pred. No. 0.12;
Matches 127; Conservative 0; Mismatches 126; Indels 3
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PRIOR FILING DATE: 2000-11-01
PRIOR PELING DATE: 2000-11-01
PRIOR PELING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 268
LENGTH: 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 268, Application US/10101464A Patent No. 6768041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              363 TGGTTGGGGAGGTACC 378
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                                                                                                                                                                                                                                                                              1843 TCCGTTCATG 1852
                                                                                                                                                                           394 ACGGCTCAAG 403
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US-10-101-464A-268
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US-10-101-464A-865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-101-464A-268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 1476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97; Indels
FILE REFERENCE: 30062-20030.00
CURRENT APPLICATION NUMBER: US/09/434,288
CURRENT PILING DATE: 1999-11-05
PRIOR APPLICATION NUMBER: 60/107,093
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38.8; DE
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Streptomyces narbonensis
US-09-434-288-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 50.0%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1101 GCAGACCCTGCTCC 1088
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US-10-101-464A-840
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US-09-434-288-12/c
US-09-434-288-12/c
Sequence 12, Application US/09434288
GENERAL INFORMATION:
APPLICANT: Bellach C., Melanie
APPLICANT: McDaniel, Robert
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Bhattramakki, Dinakar
AUTHORS: Blthon, Thomas E.
TITLE: Heat-Stress Response of Maize Mitochondria
JOURNAL: Plant Physiol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(1028)
OTHER INFORMATION: Zea Mays L., Line B73
                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (424)..(693)
OTHER INFORMATION: Heat Shock Domain
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Best Local Similarity 52.5%;
Matches 85; Conservative (
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LOCATION: (79)..(213)
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PUBLICATION INFORMATION:
AUTHORS: Lund, Adrian A.
AUTHORS: Blum, Paul H.
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(1028)..(1028)
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LOCATION: (736)..(1028)
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(329)..(1028)
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(79)..(735)
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PAGES: 1097-1110
DATE: 1998-03-00
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LOCATION: (1)...
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NAME/KEY:
LOCATION:
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LOCATION:
                                                                                                                                                                        LOCATION:
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US-10-101-464A-840

Sequence 840, Application US/10101464A

Patent No. 6786841

APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Higgins Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cell Signaling
FILE REFERENCE: 11000.10202

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2002-03-18

PRIOR PAPLICATION NUMBER: 09/704,302

PRIOR PAPLICATION NUMBER: 09/704,302

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-11-01

PRIOR PLING DATE: 1999-11-01

PRIOR PLING DATE: 2000-01-11

PRIOR PLING DATE: 2000-01-11

PRIOR PLING DATE: 2000-01-11

PRIOR PLING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 989

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    274 GCTCCCCAAGCGCGGCCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCT
CGGCGCCTCATGCTGCAGCTGGGAAGGTGTGGGAAGCGAAACAGCAAGCGGCCGCGTCGT
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4.0%; Score 38.8; DB 4;
Best Local Similarity 56.2%; Pred. No. 0.16;
Matches 73; Conservative 0; Mismatches 57;
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                                                                                                                                                                         Sequence 6, Application US/09952267B
Patent No. 6753417
GENERAL INCRRATION
GENERAL INCRRATION
APPLICANT: HANSEN, ERIC J.
APPLICANT: ABBI, CHRISTOPH
APPLICANT: OODE, LESLIE D.
APPLICANT: PREDENBURG, ROSE A.
APPLICANT: FREENBURG, ROSE A.
APPLICANT: FREENBURG, ROSE A.
TITLE OF INVENTION: USFAI AND USFA2 ANTIGENS OF WORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT FILING DATE: 2001-09-18
FRIOR APPLICATION NUMBER: US/09/336,447
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR APPLICATION NUMBER: US/09/336,447
PRIOR SEQ ID NOS: 98
SOFTWARE: PARENTIN Ver: 2.1
SEQ ID NO SECOID NOS: 98
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APPLICANT: Lund, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Moads, David M.
TITLE OF INVENTION: Isolation and Characterization of Heat Shock Protein
FILE REFERENCE: UNVN52819
CURRENT FILING DATE: 1999-02-12
EARLIER APPLICATION NUMBER: 60/076/014
EARLIER APPLICATION NUMBER: 60/076/014
SARLIER PILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Created in PatentIn Ver. 2.0, Edited in WordPerfect 6.1
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4.1%; Score 40.4; DB 4; Length 3
Best Local Similarity 46.5%; Pred. No. 0.054;
Matches 131; Conservative 0; Mismatches 151; Indels
1021 TCGGCTCTAATAATACCATTGACAGTGGCAAACAAAATGTCT 1062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Moraxella catarrhalis US-09-952-267B-6
                                                                                                                 RESULT 6
US-09-952-267B-6
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LENGTH: 1028
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US-09-249-180-1
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Sequence 6, Application US/09336447A

Sequence 6, Application US/09336447A

PAPLICANT: HANSEN, ERIC J.

APPLICANT: AEBI, CHRISTOPH

APPLICANT: COPE, LESLIE D.

APPLICANT: FISKE, MCHAEL J.

APPLICANT: F
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Pred. No. 0.054;
0; Mismatches 151; Indels 0
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Pred. No. 0.013;
0; Mismatches 51; Indels
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                                PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FLIANG DAFF: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 58.2%;
Matches 71; Conservative
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Best Local Similarity 46.5%;
Matches 131; Conservative
                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Eucalyptus grandis
FILING DATE: 1999~11-01
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                                                                                                                                                                                          SEQ ID NO 221
LENGTH: 396
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Sequence 221, Application US/10101464A

Sequence 221, Application US/10101464A

Patent No. 6768041

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT APPLICATION NUMBER: 09/704,302

PRIOR PLING DATE: 2000-11-01

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12

PRIOR APPLICATION NUMBER: 60/162,866
                                                                                                                                                                                                                                                                                                                                                                                                                                   y APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Nieuwenhuizen, Nicolaas
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101, 464A
CURRENT APPLICATION NUMBER: 09/704,302
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 2000-112
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 2000-01-11
                                 291 TIGGAGGGAICAICCCAICGICGAIIGGIGGAGCIIGAICACCIIICGCIAITIGGAICICI 350
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694 TGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAGCA 753
                                                                                                754 CAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAG
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                               Sequence 212, Application US/10101464A Patent No. 6768041 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.9%;
Matches 62; Conservative
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                                                                                                                S-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKUER, F.
APPLICANT: FALKUER, F.
APPLICANT: FALKUER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 39,72/114 IMMU
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/D7/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22313-0299
COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  243 TCGGCGGCCCTTCCC 258
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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Best Local Similarity
Matches 19; Conserv
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Sequence 6, Appli
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Sequence 12, Appli
Sequence 840, Appl
Sequence 268, Appl
Sequence 268, Appli
Sequence 268, Appli
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7635.958 Million cell updates/sec
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/cgn2 6/ptodata/1/ina/5B COMB.seg:*
/cgn2 6/ptodata/1/ina/6A COMB.seg:*
/cgn2 6/ptodata/1/ina/6B COMB.seg:*
/cgn2 6/ptodata/1/ina/PcTUS COMB.seg:*
/cgn2 6/ptodata/1/ina/PcTUS COMB.seg:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-336-44A-6
US-09-952-267B-6
US-09-249-180-1
US-09-249-180-1
US-10-101-464A-268
US-10-101-464A-369
US-10-101-464A-39
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US-10-101-464A-39
US-10-101-464A-39
US-09-228-36-15639
US-09-248-796A-2600
US-10-101-464A-31
US-09-5248-796A-2600
US-10-101-464A-837
US-09-52-596-166
US-09-072-596-171
US-09-072-596-171
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Maximum Match 100%
Listing first 45 summaries
                                                         - nucleic search, using sw model
                                                                                          October 8, 2005, 17:13:16
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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; Sequence 861, Application US/10101464A
; Patent No. 6768041
; GENERAL INPORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Strabala, Timothy
; APPLICANT: Higgins, Collean M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: Compositions Isolated from Plant Cell Signaling
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; TITLE OF INVENTION: Compositions 19010202
; CURRENT FILING DATE: 2002-01-01
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-01
; PRIOR PILING DATE: 1999-01-01
; PRIOR FILING DATE: 2000-01-10
; PRIOR FILING DATE: 2000-01-11
; PRIOR FILING DATE: 2000-01-11
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFFWARE: FastSEQ for Windows Version 4.0
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48.4%; Pred. No. 0.002;
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                         US-09-249-180-7

US-09-270-767-12912

US-09-902-540-865

US-10-101-464A-841

US-09-105-537-30

US-09-105-537-30

US-09-105-537-30

US-09-105-537-30

US-09-105-537-30

US-09-105-537-30

US-09-11-908-1

US-09-336-447A-10

US-09-336-447A-10

US-09-952-2678-10

US-09-952-2678-10

US-08-567-375-1

US-08-567-375-1

US-08-567-375-1

US-09-134-000-2219

US-09-144-000-2219
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ORGANISM: Eucalyptus grandis
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US-10-101-464A-861
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SEQ ID NO 861
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Sequence 268, App Sequence 39, App Sequence 39, Appl Sequence 421, Appl Sequence 15639, A Sequence 15639, A Sequence 17, Appl Sequence 17, Appl Sequence 166, Appl

Sequence 2, Appli Sequence 1, Appli Sequence 34, Appl

US-09-103-840A-2 US-09-103-840A-1 US-09-105-537-34

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Sequence 34, Sequence 5, A Sequence 19, Sequence 1, A

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Search completed: October 8, 2005, 19:58:39 Job time: 3177 secs

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Secale cereale cDNA clone Sc02_07e09, mRNA sequence.
Site_1: EcoRI; Site_2: XhoI; Seeds were germinated and grown at 4 C for 5 weeks. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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1 (bases 1 to 703)

3 ingh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A. Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings Unpublished (2000)
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/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI; Site_2: Xho I; Sampled three-leaf seedlings treated for cone week at 2oC, 12 hrs light/day. Library made with Stratagene UNIZAP XR Kit/(not packaged). cDNA is directly ligated into SK+/XhoI-EcoRI, then electroporated into
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/clone="cc02_07e09"
/closue_type="leaf, crown"
/dv_stage="seedling three-leaf stage"
/clone_lb="sc02_AAFC_ECORC_cold_stressed_winter_rye_seedlings"
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Contact: Singh,J.A.

Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Oti
0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhj@agr.gc.ca.
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/mol_type="mRNA"
/cultivar="Puma (winter rye)"
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Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
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1 (Dases 1 to 692)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., The structure and function of the expressed portion of the wheat genomes - Vernalized crown cDNA library
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                                                                                                                                                                                                                                                                                                                               ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT 691
                                                                                                                                                                                                                                                                                                                                                                             324 ACCGTAACTGGTAGCAACCATGTCGTATCTGGGGACAAACATATCGTAACTGACAACAAC
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  564 CGCCTCAAGGGCTTCGCCATCGCTGGTCGTTCATCAGGTATGATTTTTACTAACATGCCA
                                                  TTGCATGT - - - GAGCAGTAGAAGAACGCTCGATGAAGAACCAAATACAATATCAGGGACC
                                                                          504 TIGTATGTGGGGCCTAACAGAAGAATGCTCGACGAACAACAAATACAATATCTGGGGGC
                                                                                                                                             AACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAATGACAACACGGTCGTA
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WHE0840_D01_H02ZS Wheat vernalized crown cDNA library Triticum
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/lab_host==E. coli SOLM:
/lone_lib="Wheat vernalized crown cDNA library"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
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Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers

    692
    organism="Triticum aestivum"

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BF474043.1 GI:11543225
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Hordeum.
1 (bases 1 to 689)
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AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAG
                                                                                                                                                                                                              446 AATGCCGTATCCGGGAATGACAATAATGTATCTGGGAGTTTCCATACCGTATCCGGAAGC
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                                                                          ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT
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Akashimriki vegetative stage leaves"
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Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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Location/Qualifiers
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BJ458121
BJ458121.1 GI:21136659
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BJ450137 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak28d17 5', mRNA sequence.
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (Bases I to 609)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
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                          202 ATCCGGAAGCCACAATACTGTATCTGGGACCAACAACACTGTATCTGGGAACAACATGT 143
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ATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATAT
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/clone lib="K. Sato unpublished cDNA library, cv.
Akashinriki vegetative stage leaves"
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                                                                                        CGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAATAT 841
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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
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Location/Qualifiers
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    BJ462238 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baakstagl6 3', mRNA sequence.
BJ462238 I GI:21140745
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                                                                                                                                                        Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Hordeum.
1 (bases 1 to 684)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 GAACGACAATACCGTAACTGGTAGCAACCATGTCGTATCTGGGGACAACATATCGTAAC
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| db_xref="texaon:112509"
| db_xref="texaon:112509"
| fissue_type="leaves"
| dev_stage="vegetative stage"
| dcome_lib="K. Sato unpublished cDNA library, Akashimiki vegetative stage leaves"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 684;
                                                                                                                                                                                                                                                                       Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Akashinriki"
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                                                                                                                                                                                                                                                                                                                                                 Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 357.6; DB 4;
Pred. No. 1.5e-95;
0; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 36.5%; al Similarity 78.4%; 455; Conservative
                                                                                                                                         EST
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Best Local S
Matches 455
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                                                                                          ACCESSION
VERSION
KEYWORDS
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296 GGGATCATCCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGT 355
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                                                                                                                                                                                                                                /sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baak46n01"
/tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
                                                                                                                                                                                                                                                                                                                                                                                               671;
                                                                                                                                                                                subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                              Score 359.4; DB 4; Length
Pred. No. 4.2e-96;
0; Mismatches 136; Indels
                                                                    Shizuoka 411-8540, Japan
            Contact: Tadau Shin-i
Contact: Tadau Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Jap
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
Location/Qualifiers
                                                                                                                                                                          /organism="Hordeum vulgare
/mol_type="mRNA"
/cultivar="Akashinriki"
                                                                                                                                                                                                                                                                                                                                                                                            tch 36.7%;
al Similarity 76.7%;
467; Conservative (
Unpublished (2002)
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Best Local Similarity
Matches 467; Conserv
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BJ462238/c
JOURNAL
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 671)
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                                                                                                                                                                                                                                                                     CATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCTCGGGTAATTC
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                /tissue_type="leaves"
/dev_stage="vegetative stage"
/clone_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
                                                                                                                          Length 632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
                                                                                                                                                             Indels
                                                                                                                        Score 362.2; DB 4;
Pred. No. 6e-97;
0; Mismatches 133;
clone="baak42e04"
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BJ454271.1 GI:21132845
                                                                                                                    37.0%;
ilarity 77.1%;
Conservative 0
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Matches 468;
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BJ452251 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak2e04 5', mRNA sequence.
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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaee; Hordeum.
1 (bases 1 to 632)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
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257 CGCGTCGTGGCGTTGCGGCTCCCCAAGCGCGGCCTTGGAGGGATCATCCCATCGTCGATT

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/organism="Hordeum vulgare"

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Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
1181 81-559-81-6856
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/sub_species="vulgare"
/db_xref="taxon:112509"
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Location/Qualifiers
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I (basea: Triticeae; Triticum.

I (basea: Lo. 588)

Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., The structure and function of the expressed portion of the wheat genomes - Cold-stressed seedling cDNA library
                                                                                                                    916
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                                           146 AGCAACAAAGTCGTAGGAGATGCATGATTTGTAAGTGGAGTGTCCATCTTCCGTGACGAA
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Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
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Triticum aestivum
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Fax: 5105595818
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                                                               /sub_species="vulgare"
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Akashinriki vegetative stage leaves"
                                                                                                                                                                                         Score 365.6; DB 4;
Pred. No. 5.9e-98;
0; Mismatches 144;
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                                       /mol_type="mRNA"
/cultivar="Akashinriki"
Location/Qualifiers
                                                                                                                                                                                         Query Match
Best Local Similarity 75.3%;
Matches 503; Conservative
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BJ461908 K. Sato unpublished cDNA library, cv. Akashinriki BJ461908 K. Sto unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak21d01 3', mRNA sequence.

BJ461908/c LOCUS DEFINITION

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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticaee; Hordeum.

1 (bases I to 696) and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

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Pred. No. 5.9e-98;
0; Mismatches 144; Indels
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/dev_stage="vegetative_stage"
/clone_lib="K. Sato_unpublished_cDNA
Akashinriki vegetative_stage_leaves"
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/cultivar="Akashinriki"
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/db_xref="taxon:112509"
/clone="baak21d01"
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Location/Qualifiers
GI:21140417
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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticae; Hordeum.

El (bases) Iro 693)

Sato, K., Saisho, D. and Takeda, K.

Barlo, E. Saisho, D. and Takeda, K.

Barlo, E. Sassoning project in NIG and Okayama Univ

Unpublished (2002)

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AUTHORS
TITLE
JOURNAL
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/ organism="Hordeum vulgare subsp. vulgare"
/ organism="Hordeum vulgare subsp. vulgare"
/ mol type="mRNA"
/ cultivar="Akashinriki"
/ sub species="vulgare"
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1 (bases I to 699)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
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                  CTCCCCAAGCGCGCCCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTT
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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Location/Qualifiers
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Establishes; Lo 686)

Sato, K., Saisho, D. and Takeda, K.
Barley Est sequencing project in NIG and Okayama Univ Unpublished (2002)

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Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Hordeum.

E 1 (bases 1 to 746)

S ato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

L Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81.6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BJ458554 746 bp mRNA linear EST 23-MAY-2002 BJ458554 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak32116 3', mRNA sequence.
BJ458554 GI:21137090
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Location/Qualifiers
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Email:
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BJ461731 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak46120 3', mRNA sequence.
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                            Indels
Score 372.4; DB 4;
Pred. No. 5.5e-100;
0; Mismatches 166;
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3228.8
3258.8
3252.2
3318.6
3316.2
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       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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BJ451048 K. Sato unpublished cDNA library, cv. Akashinriki vegetative stage leaves Hordeum vulgare subsp. vulgare cDNA clone baak32116 5', mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases; Triticeae; Hordeum.
1 (bases; Triticeae; Hordeum.
2 (bases I to 767)
Saloo, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
                                                                                                            AV910970
FGAS03708
AV911379
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/clone_lib="K. Sato unpublished cDNA library,
Akashinriki vegetative stage leaves"
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Tel: 81-559-81-6856
Fax: 81-559-81-6855
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/db_xref="taxon:112509"
/clone="baak32h16"
/tissue_type="leaves"
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/cultivar="Akashinriki"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
                       BJ447068
AV909087
BJ454200
CK197682
BE705684
                                                                                     BJ453816
AV3100903
AV911379
BM376551
BM37653
BM37653
BM37653
BM376325
AJ460325
CK196896
CK196896
CK196896
AJ460320
AJ460320
BJ460799
BJ456413
                                                                                                                                                                                                                                                                                                                                                                                                       BJ451048
BJ451048.1 GI:21129647
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Best Local Similarity 73.5
Matches 524; Conservative
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incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high mutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence represents a plant mucleic acid of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 AAGCGCGCCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTAT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 gecháddak decentración de 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 GGGCGAGGTCTCGAGGGGCCCATCCCGCCCTCGCCGCCCTCGCGCGCCTCCAGGAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 GCAACGTCGTGGTCGTGCCACCACGACGTCCACGCGTTGAGGGGCCTCGCTGAGAAC
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8.1%; Score 79.4; DB 12; Length 4536;
Best Local Similarity 63.1%; Pred. No. 2.2e-13;
Matches 157; Conservative 0; Mismatches 86; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4536 BP; 1102 A; 1247 C; 1221 G; 965 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGGATCIC 349
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Search completed: October 8, 2005, 17:53:50 Job time : 580 secs

681

851

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The invention relates to plant nucleotide sequences that direct seed, leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential cor constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is altered in the seed, leaf, stem, panicle, pollen, root or is constitutive in a plant cell. The plant is a creal, e.g. soybean, alfalfa, sunflower, canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, sorghum, rice or wheat. The polymucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve phenotypic characteristics, to produce large quantities of oil or proteins, to incur resistance to insecticides, viruses or fungi, and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral; antifungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value.
682 aaraccerarchedeaaaaacaarrccerarareeeaacaacaararrere
                                                                                                     CATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAATATTCTGTAGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 25; SEQ ID NO 1496; 230pp; English.
                                                                                                                                                                                                                                                                                                                                             BP.
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Katagiri F, Kreps J,
                                                                                                                                                                                                                                                                                                                                             ADJ40496 standard; cDNA; 4536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001; 2001US-0325277P.
26-SEP-2001; 2001US-0325448P.
04-APR-2002; 2002US-0370620P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BUDWORTH P.
MOUGHAMER T.
BRIGGS S P.
COOPER B.
GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-190374/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KREPS J.
PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant cDNA #1496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2004016025-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota
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(PROV/)
(RICK/)
(ZHUT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLAZ/)
(GOFF/)
(KATA/)
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(BRIG/)
(COOP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BUDW/)
                                                                                                                                                                                                                                                                              RESULT 15
                                                                                                                                                                                                                                                                                                             ADJ40496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is that of cDNA encoding AFP1, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a pseudostem cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides contains and the polynucleotides encoding them ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promect. Sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The cantifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of amblecular biology creagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCACTGGGTATGGGT 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               737 ACTGTATCAGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAAC 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antifreeze proteins and encoding polynucleotides, useful for lating cold tolerance in organisms, as food additives, or for ating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 TTCACTCACATGCCATTACATGTGAAGCCTAGCCAAGGAACACTCGACGAAGACCACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 262.2; DB 12; Length 841; Pred. No. 3.1e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 841 BP; 216 A; 217 C; 222 G; 186 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protect a plant from damage due to frost or freezing.
                                                                                                                                                                                                                                                                                                                 Fish SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 1; 71pp; English.
                                                                                                                                                                                                           (GENE-) GENESIS RES & DEV CORP LTD. (WRIG-) WRIGHTSON SEEDS LTD.
                                                                                                                                                                                                                                                                                                                 Hall C,
                                                                         09-SEP-2003; 2003WO-NZ000199
                                                                                                                                               09-SEP-2002; 2002US-0409557P
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Best Local Similarity 73.5%;
Matches 349; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biocrystals (e.g. gout).
                                                                                                                                                                                                                                                                                                                 Demmer J, Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                            WPI; 2004-248453/23.
P-PSDB; ADM41471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antifreeze p
modulating cold
              18-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  440
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confectionery. Anti-freeze proteins are especially used in food products, which are heated, e.g. by pasteurisation, blanching or sterilisation prior to freezing. Plants transformed with a nucleic acid sequence and anti-freeze protein have an increased frost tolerance. Prior ant anti-freeze proteins have not been applied to commercially available food products, due to high costs and complicated processes for obtaining the protein. Also prior art anti-freeze proteins have tended to destabilise during processing especially during the pasteurisation step. This is overcome by the present anti-freeze protein. The anti-freeze protein anti-freeze or anti-freeze protein and inhibition assay of 15 mu M or less. The anti-freeze protein ingredient means that mixes can be frozen under quiescent conditions, e.g. in a shop or home freezer without the formation of unacceptable ice crystal shapes and hence with a texture different to products normally obtained via
                                                                                                                                                                                                                                                                                                                                                                                           TCCGGGAGCTTTCATACCGTATCCGGGGGCACAATACTGTGTCCGGGAGCAACAATACC 300
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                                                                                                                                                                                                                                                            Length 357;
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Pred. No. 4.4e-72;
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                                          AGTITCCAGATATTGCTCAAGGCTTCACCACGCTGGCCGTTCACTGGGTAAGGCGTTC
                                                                                        ACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACT
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Library. The invention provides forage grass (peremial ryegrass and tall lescue. The invention provides forage grass (peremial ryegrass and tall library. The invention provides forage grass (peremial ryegrass and tall lescue.) ADM41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold cold cold cold and parts. The method involves incorporating an antifreeze of polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting to the polynucleotide into the cells of the organism, thereby inhibiting cold grown of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is that of cDNA encoding an antifreeze protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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Pred. No. 8.7e-74;
0; Mismatches 116;
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                ADM41459 standard; cDNA; 959
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142. .810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 74.8
Matches 353; Conservative
                                                                                                                                                                                              Schedonorus arundinaceus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biocrystals (e.g. gout)
                                                                                                                                                                                                                                                                                                                           142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shenk MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-248453/23.
P-PSDB; ADM41472.
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                                                                               03-JUN-2004
                                                                                                                                                              litholytic;
                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                           mat_peptide
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                                                                                                         106 TGGCCATGAĞCGCGAÇ----ĞTCGTĞCCACCTGGATGACCTCCGCGCGCTGCGGGGCT 159
                                                                                                                                                                                                                                                        GGCTTCCGATTAGCCTCGAGGACTGCGGTAAGCTCCAAGTCGCTCAACCTTGCCAACGAAA 336
                                                                                                                                                                                                                                                                              288 GCCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATC 347
                                                                                                                                                                                                                                                                                                                               TCTCGGGTAATTCATTGGTTGGGGAGGTACC------AAAAAGTTTGCAGATAC 395
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                                                                                                                                                                                                                                 GGCTCC-------CCAAGCGCG 287
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                                                           46 ccagaactraarccareeceaaarerreecrecrecrecrerrerreererrecrerrec
                                                                                    <u> AGGTGGCAGGAGCAACGTCGTGGTCGTGCCACCACGACGACCTCCACGCGTTGAGGGGCC</u>
                                                                                                                                                                                              GATTGGTTGCACCATCCCGTCGTGGATTGGTGAGCTTGACCACCATTGCTACTTGGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCAACAAACTCGTGACAGGAGATGATTGTTTGTCAGGGGATTGCTTCCATCTTTCCTAA
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                                                                                                                                                                                                                                                                                                                                               ACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGA
                                                                                                                                                160 TTGTCGGGAACCTCAATGGC---GGGGGGTGCCCTTCTCCGTGGAACATGGTCTGGCTCCT
                                                                                                                                                                                                                                                                                                                                                                               GGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGGTTCCATTAACATGCTAT
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                                    CCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGGTCTTCTTGGGGTTCATCTTGC
                                                                                                                                 TCGCTGAGAACCTAAGCGGCAAAGGAGCCGTCCGCCTCCGCGCCCGCATGGTCCGGCGCCT
             Gaps
            90;
             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTTATGTAACTTCA-GGATATGGCATACTTTTCCTT 948
Pred. No. 6e-120;
0; Mismatches 206;
70.3%;
            701; Conservative
 Best Local Similarity
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            Matches
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The present sequence is that of cDNA encoding AFP4, an antifreeze protein of perennial ryegrass. The CDNA was isolated from a leaf and pseudostem CC of perennial ryegrass. The CDNA was isolated from a leaf and pseudostem cCC constant interest of the invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides controlled from tissues taken at different times of year (winter and spring) and from different parts of the plants. The plynucleotides can be used to condition the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded CRNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a control or a disorder characterised by biocrystals associated with disorders such as a disorder characterised by biocrystals associated with disorders such as a because the control or a method for the control or antifreeze protein can be used by associated with disorders such as a disorder characterised by biocrystals associated with disorders such as a disorder characterised by biocrystals associated with disorders such as a disorder characterised by biocrystals associated with disorders such as a disorder characterised by biocrystals associated with disorders such as a disorder characterised by biocrystals associated with disorders such and a disorder characterised by biocrystals associated with disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                          Antifreeze, perennial ryegrass; cold tolerance; transgenic; plant; antigout; litholytic; nephrotropic; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1064 BP; 263 A; 274 C; 267 G; 260 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Antifreeze protein AFP4"
                                                                                                                                                                                                                                                                             Perennial ryegrass antifreeze protein AFP4 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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BP
ADM41465 standard; cDNA; 1064
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/product= '
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121. .894
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Sequence 1084 BP; 290 A; 258 C; 262 G; 274 T; 0 U; 0 Other;
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                        RESULT 10
ADM41462
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                                                                                                                               AGGTGGCAGGAGCAACGTCGTGGTCGTGCCACCACGACGTCCACGCGTTGAGGGGCC 152
                                                                                                                                                                                                                                                                                                                     276 GCTTCCGATTAGCCTCGAGGACTGCGGTAAGCTCAAGTCGCTCAACCTTGCCAACGAAA 335
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                                                    Gaps
                                                   90;
                          Length 1083;
290 A; 257 C; 262 G; 274 T; 0 U; 0 Other;
                                                   Indels
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                                                   205;
                       Score 419; DB 12;
Pred. No. 1.9e-120;
0; Mismatches 205;
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                       ch 42.8%;
il Similarity 70.4%;
702; Conservative
  Sequence 1083 BP;
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The present sequence is that of cDNA encoding AFP3, an antifreeze protein

of perennial ryegrass. The cDNA was isolated from a root cDNA expression

library. The invention provides forage grass (perennial ryegrass and tall

fescue) antifreeze proteins and the polymucleotides encoding them

ADM41458-ADM41483. The polymucleotides were isolated from tissues taken

at different times of year (winter and spring) and from different parts

of the plants. The polymucleotides can be used to modulate the cold

colerance of an organism, especially plants, mammals, insects, fungi,

colerance of an organism, or introducing only estimate and bacteria. The method involves incorporating an antifreeze

polymucleotide, under the control of a gene promoter sequence, into the

genome of the organism, or introducing double-stranded RNA corresponding

corpression of an antifreeze polypeptide. The antifreeze protein can be

used for the cryopreservation of a cell or tissue, as a food additive of

a frozen food product, in a method for decreaning the time required to

composition, to treat a disorder characterised by biocrystals

cassociated with disorders such as gout and kidney stones, to presserve the

viability of a molecular biology reagent, to destroy unwanted tissue in a
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                                                                                                                                                                                                                                                                  Antifreeze, perennial ryegrass, cold tolerance, transgenic, plant, antigout, litholytic, nephrotropic, cytostatic, gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Antifreeze protein AFP3"
                                                                                                                                                                                                  protein AFP3 cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                     Perennial ryegrass antifreeze
standard; cDNA; 1084
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60. .117
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P-PSDB; ADM41475.
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Length 1084;

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viability of a molecular biology reagent, to destroy unwanted tissue in patient e.g. tumour tissue, and to protect a plant from damage due to
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                                                                                                                                                                              Gaps
                                                                                                                                   DB 12; Length 1246;
                                                                                                                                                                            Indels 103;
                                                                                        Sequence 1246 BP; 313 A; 294 C; 307 G; 332 T; 0 U; 0 Other;
                                                                                                                                 Score 421.8; DB 12;
Pred. No. 2.7e-121;
0; Mismatches 192;
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Matches 690; Conservative
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frost or freezing.
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The present sequence is that of cDNA encoding, an antifreeze protein of perennial ryegrass. The invention provides forage grass (perennial companies) of ryegrass and tall feacue) antifreeze proteins and the polymucleotides compound the ADM41458-ADM41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from companies, fungi, archaea and bacteria. The polymucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating companies polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, contrared inhibiting expression of an antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for contrast as a food additive of a frozen food product, in a method for theories as a food additive of a frozen food product, in a method for contrast and kidney stones, to preserve the viability of a molecular biology to reagent, to destroy unwanted tissue in a patient e-g. tumour tissue, and contracted a plant from damana dissue in a patient e-g. tumour tissue, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
                                                                                                                                                                                                                                                       Antifreeze, perennial ryegrass, cold tolerance, transgenic, plant, antigout; litholytic; nephrotropic, cytostatic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protect a plant from damage due to frost or freezing.
                                                                                                                                                                                                                                                                                                                                                                                          'product= "Antifreeze protein'
                                                                                                                                                                                                                       Perennial ryegrass antifreeze protein cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fish
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                   1017 TCATGGGATATATCATACCTTTCCT
 TCA--GGATATGGCATACTTTCCT
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a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and to protect a plant from damage due to
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The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The CDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue. The cDNA was isolated from a leaf blade cDNA expression continuous and the polynucleotides encoding them to ADMA1458-ADMA1483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the polynucleotides can be used to modulate the cold cold archaea and bacteria. The method involves incorporating an antifreeze polynucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polynucleotide into the cells of the organism, thereby inhibiting contending to the polynucleotide into the cells of the artifreeze protein can be expression of an antifreeze polypeptide. The antifreeze protein can be a frozen food product, in a method for decreasing the time required to a frozen food product, in a method for decreasing the time required to associated with disorders such as gout and kidney stones, to preserve the
 925
                              995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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                   CTTGTCCAAGTTCAGTGCAGCTCACAATCACTTGGTAGGGGCAATCGAGTTATGTAACTT
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                                                                                                                                                                                                                                                                                                                                                                       Antifreeze, perennial ryegrass, cold tolerance, transgenic, plant, antigout; litholytic; nephrotropic; cytostatic; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1007 BP; 252 A; 265 C; 253 G; 237 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.3%; Score 492.8; DB 12; Best Local Similarity 73.6%; Pred. No. 1.2e-143; Matches 739; Conservative 0; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 TCTTCTTGGGGTTCATCTTGCAGGTGGCAGGA------
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                                                                                                            TGTAGCTTACAATCAATAGATGGAGACAATCACGTTATGTAACTTCA-GGATATGGCATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
---CCCAAGTTCAG
                                                                                                                                                                                                                                                                                                                                                       fescue; cold tolerance; transgenic; plant; antigout; nephrotropic; cytostatic; gene; ss.
                                                                                                                                                                CTTTTC---CTTTAAATAAGCTTCCCTTTACATAAAAAAA 980
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ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADM41483. The polymucleotides were isolated from clissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to condulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating con antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze protein can be used for the cryopresservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a patient e.g. tumour tissue, and
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                                                                                                                                                                                                                                                                     TCAGCGCATGATTGTTTCCACCTTAACTGAGCTCACGTTCTTGTCCAAGTTCACTGTACC 910
                                                                                                                                                                                                                                                                                                                                                                                         TCACAGTCAGTTGGTGCGTTCAATCGCGTTATGTAACTTCATGGATATACCATACTTTTC 970
                                                                                                                                                                                                                                                                                                                               TTACAATCAATAGATGGAGACAATCACGTTATGTAACTTCA-GGATATGGCCATATTT
GGAGCTTTCATACCGTATCCGGGGGCACAATACTGTCTCCGGGAGCAACAATACCGTAT
                                                                                                                                                                                                              TAGGTGCAGGATTGCTTCCATCTT---------CCCAAGTTCAGTGTAGC
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GAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTAT

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The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression collibrary. The invention provides forage grass (peremial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them compared and the polymucleotides encoding them compared times of year (winter and spring) and from different parts of the plants. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polymucleotides can be used to modulate the cold colerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the collymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide into the cells of the organism, thereby inhibiting to the polymucleotide, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a control of a plant from damage due to
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Sequence 1006 BP; 248 A; 261 C; 260 G; 237 T; 0 U; 0 Other;

9 555 558 615 618 675 678 TTCCATTAACATGCTATTGCATGTGA---GCAGTAGAAGAACGCTCGATGAAGAACCAAA 495 rrrcaccaacareccarrecarereareceraacaeaaearcacreeaeeaeeaeceaa 498 GITCATCTTGCAGGTGGCAGGA---GCAACGTCGTGGTCGTGCCACCACCACGACGTCCT 138 207 258 267 318 378 AAAAAGTTTGCAGATACGGCTCAAGAGCCTCACCACTGACAGCCAGTCACTCGGTATGGG 438 388 caagaarcriccaggracagcricaaaggccricacggricccggric------grrcgg 438 268 reficaceecrificacerceccaeaeceecercaceeeccaarcecarcearing 327 328 rcagcircaccacciacciacircacircairciricaddiaarigcariggirggcdaddiaca 87 TACAATATCTGGGAGCAACAATACTGTCAGATCCGGGAGCAAAAATGTTGTTGCTGGGAA TGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCA TACAATATCAGGGACCAACAATAGTGTTGGATCAGGGAGCAACAATGTTGTTTCCGGGAA AACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATAT 208 GIGGTCAGGCGCCTCAIGCIGCGATIGGGAAGGCGTIGGCTGCGACGCIGCAGCGGCGCCG AAGTGGGAGTGACAATACCGTAACTGGCAGCAACCATGTCGTATCAGGGACAAACCATAT TCTTGTTCAATCCATGCCTGAATACATGGCAAAGTGTTGCATGCTGCTGGTCTTCTTGGG 199 ATGGTCCGGCCCTCATGCTGCAGCTGGGAAGGTGTGGGAAACAGCAAACAGCGGCCG CGTCGTGGCGTTGCGGCTCCCCAAGCGCGCCTTGGAGGGATCATCCCATCGTCGATTGG 28 reraragearageacrectearecearegegaargerrearecrecrecerecerede Gaps 55.3%; Score 541.6; DB 12; Length 1006; 76.5%; Pred. No. 5.3e-159; 38; Indels 0; Mismatches 194; 756; Conservative Best Local Similarity Matches 756; Conserv 259 379 919 22 319 439 499 559 616 619 82 439 496 556 88 Query Match g g ò 임 유 g g g ò 8 ð ò 셤 8 d g g ò ઠ ઠે ઠે ò

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The present sequence is that of cDNA encoding AFP5, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial
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                                                                                                                                                                                        ----CCCAAGTTCAGTGTAGCTTACAATCAA
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                                                                                                       TACCGTATCCGGGGGGCACAATACCGTCTCTGGGAGCAACAATACCGTATCTGGGAGCAA
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                                                       TACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGG
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P-PSDB; ADM41480.
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(WRIG-) WRIGHTSON SEEDS
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                            The present sequence is that of cDNA encoding an antifreeze protein of tall fescue. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polynucleotides encoding them fescue) antifreeze proteins and the polynucleotides encoding them ADN41458-ADM41483. The polynucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The polynucleotides can be used to modulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded RNA corresponding expression of an antifreeze polypeptide. The antifreeze protein can be used for the cryopreservation of a cell or tissue, as a food additive of a frozen food product, in a method for decreasing the time required to dehydrate a composition, to treat a disorder characterised by biocrystals associated with disorders such as gout and kidney stones, to preserve the viability of a molecular biology reagent, to destroy unwanted tissue in a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 996 BP; 268 A; 235 C; 250 G; 243 T; 0 U; 0 Other;
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Pred. No. 5.2e-273;
ID NO 4; 71pp; English.
SEO
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834
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TAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAA
                                              TAATGTGTCTCGGGAGCTTCCATACTGTATCAGGGGAGCACAATACCGGTATCTGGGAGCAA
                                                                                                                   CAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fescue, cold tolerance, transgenic, plant, antigout, nephrotropic, cytostatic, gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCTTCCCTTTACATAAAAAAAA 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  967 AAGCTTCCCTTTACATAAAAAAA
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960

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780

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601 CAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATC
                                                                                                                                                                                                                                                             TGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAAACAGTTGTTAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted biocrystals (e.g. gout).
                                                                                                                                                       GTCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATACCGTATCCGGGAGCAACAATAC
                                                 AGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGT
                                                                                fescue; cold tolerance; transgenic; plant; antigout;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
41. 850
/*tag= b
/product= "Antifreeze protein"
/transl_except= (pos:410. .412,aa:Xaa)
/note= "Xaa= unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nephrotropic; cytostatic; gene; ss
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                                                                                                The present sequence is that of cDNA encoding AFP2, an antifreeze protein of perennial ryegrass. The cDNA was isolated from a leaf blade cDNA expression library. The invention provides forage grass (perennial ryegrass and tall fescue) antifreeze proteins and the polymucleotides encoding them ADM41458-ADN41483. The polymucleotides were isolated from tissues taken at different times of year (winter and spring) and from different parts of the plants. The plymucleotides can be used to condulate the cold tolerance of an organism, especially plants, mammals, insects, fungi, archaea and bacteria. The method involves incorporating an antifreeze polymucleotide, under the control of a gene promoter sequence, into the genome of the organism, or introducing double-stranded CC RNA corresponding to the polymucleotide into the cells of the organism, thereby inhibiting expression of an antifreeze polymelectic into the cells of the organism, can tissue, as a food additive of a frazen food product, in a method for decreasing the time required to dehydrate a composition, to treat a composite as a food additive of a frazen food product, in a method for descreasing the time required to dehydrate a composition, to treat a composition, to destroy unwanted tissue in a patient e.g. tumour tissue, and content a plant from damage due to frost or freezing.
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100.0%; Score 980; DB 12; Length 980;
Best Local Similarity 100.0%; Pred. No. 9e-297;
Matches 980; Conservative 0; Mismatches 0; Indels 0
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                                                            Claim 1; SEQ ID NO 3; 71pp; English
           (e.g. gout)
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ABA17080 Drosophil
Ab17070 Drosophil
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Ab563672 Human kid
Ab563672 Human kid

Abz23668 H. pylori Abl17081 Drosophil Abl17080 Drosophil Aaa50251 Maize hea

Minimum DB Maximum DB

Database

Result 8

Searched:

Sequence:

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New antifreeze proteins and encoding polynucleotides, useful for modulating cold tolerance in organisms, as food additives, or for treating tumors or disorders associated with the presence of unwanted
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/product= "Antifreeze protein AFP2"
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P-PSDB; ADM41473.
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Adm41458 Perennial
Adj40496 Plant cDN
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Search completed: October 8, 2005, 19:05:38 Job time : 4305 secs

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15 Marzup, Danzie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allan, H., Alsbrooks, S., Amin, A., Angulano, D., Allan, H., Alsbrooks, S., Amin, A., Angulano, D., Allan, T., Alsprooks, S., Amin, A., Angulano, D., Allan, H., Alsbrooks, S., Amin, A., Barnstead, M., Benahmed, F., Balar, D., Bandsteil, M., Barnstead, M., Benahmed, F., Balawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bandshon, D., Bandsteil, B., Barnstead, M., Benahmed, F., Brawalo, C., Blair, J., Bursal, R., Chen, Z., Chu, J., Chacko, J., Chare, D., Chang, C., Burnel, P., Burnel, R., Chen, Y., Chen, Z., Chu, J., Chacko, J., Chare, D., Chang, S., Dun, H., Diya, K., Chang, C., Daylogo, O., Denson, S., Davy, Ccarcoll, L., Da Anda, B., Esres, K., Esper, H., Daylan, Rochas, D., Chang, R., Mand, S.L., Hodgson, A., Hodgson, A., Hodgson, A., Hodgson, A., Hodgson, A., Hodgson, A., Havlak, P., Haves, S., Hulyk, S., Hune, V., Mand, S., Kelly, R., Mand, M., Mand, 
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23908282.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
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may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 TAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          640 TGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGT
                                                                                                                                                                                                                                                                Assembly program: Phrap; version 0.990329
Consensus quality: 165932 bases at least Q40
Consensus quality: 167952 bases at least Q40
Consensus quality: 167961 bases at least Q20
Estimated insert size: 169210; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 172927;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 52.4%; Score 59.6; DB 2; Length 1 Similarity 52.4%; Pred. No. 0.00021; Sift Conservative 0; Mismatches 119; Indels
                                                                                                        /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-462N7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="clone_boundary clone_end:T7
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/note="wgs end_extension clone_end:Sp6"
1305. .2525
/note="wgs end_extension clone_end:Sp6"
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/note="wgs_end_extension
clone_end:T7"
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complement(167491..160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence:BZ144777"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1190. . . 4089 /note="clone boundary clone end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
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misc_feature
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                                                                                                                                                                                                                                                                                                                                       source
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AC119701/c
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SOURCE
ORGANISM
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DEFINITION
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VERSION
                                                                                                                                                                                                                                                                                                   FEATURES
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Submitted (10-MAY-2003) Human Gencemes Sequencing Center, Department of Mondecular and Human Genceites, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819414.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Bach contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the entime to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome extend as sequences and whole genome
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Sher, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svarek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, C., Wallson, R., Waldron, L., Walker, R., Wang, J., Wijht, D., Wailson, R., Wlezy, K., Wooden, H., Worley, K., Wright, D., Wright, R., Wals, S., Yen, J., Yakub, S., Yen, J., Yoon, U., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (04-JUG-2002) Human Genome Sequencing Center, Department
Submitted (04-JUG-2002) Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 261587)
Rat Genome Sequencing Consortium.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a "working draft" sequence. It currently

* consists of 7 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Assembly program: Atlas 3.0;
Consensus quality: 245312 bases at least Q40
Consensus quality: 249138 bases at least Q30
Consensus quality: 25121 bases at least Q20
Estimated insert size: 257796; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shotgun sequence only contigs will be indicated in the feature table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250010: contig of 250010 bp in length 250110: gap of unknown length 253467; contig of 3357 bp in length 253567; gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project Information
Center project name: GHUJ
Center clone name: CH230-104014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 261587)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Worley, K.C.
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253468
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AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
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JOURNAL
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COMMENT

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83693 T-----GTATCAGCACTGTGTTAACATGTATCAGCACTGTTGTAGCATGTATCAGCACT 83640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83579 ACTGTTGTAGCATGTATCAGCACTGTGTTAACATGTATCAGCACTGTTGTAGCATGTATC 83520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83753 ATCAGCACTGTTGTAGCATGTATCAGCACTGTTGTAGCATGTATCAGCACTTTTGTAGCA 83694
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Rattus norvegicus clone CH230-462N7, WORKING DRAFT SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     752 CACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGG 811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                632 ACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCATATTGTTACTGATAACAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     572 TCTGGGAATAACAACCATGTGTCTGGGAGCAACACACTGTTGTAACTGGAAGTGACAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 261587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                             249 256807: contig of 1559 bp in length 1808 256907: gap of unknown length 1808 2568685: contig of 1678 bp in length 1858 2568685: gap of unknown length 166 260166: contig of 1481 bp in length 167 26026: gap of unknown length 167 261587: contig of 1321 bp in length 167 261587

| Coation/Qualifiers | 1321 bp in length 16587 |
| Coganism="Rattus norvegicus" |
| Amol type="genomic DNA" |
| Aref="taxon:10116" |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.2%; Score 60.8; DB 2; Length 2.
Best Local Similarity 51.9%; Pred. No. 0.00011;
Matches 165; Conservative 0; Mismatches 147; Indels
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HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .247488)
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clone_end:\bar{T}"
6414
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/note="wgs_end_extension
clone_end:T7"
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complement(246622..24
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/note="clone_boundary
clone_end:T7
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contig c
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site:EcoRI
                            255248:
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258686
260167
260267
                      255149
255249
256808
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233583 GTTATTACAATATTGTTCATGGTTATTATAATATTGTTCAGGGTTATTACAATATTGTTC 233642
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DLONQLESGIIPDDFKRQMFYTFGDYRDFLFGTDISKGHGIGSELAKKIDSLFKNIGG
KUPGDLSKOWNENGPYTWRGMLCZELKAWGFOTTKNKSYNYTHNYRSDNRNGPDL
KUPGDLSKOWNENGPYTWRGMLCZELKAWGFOTTKNKSYNYTHNYRSDNRNGPDL
KUPGDLSKPRENGERECENGKQLDILKKKCPKETCTPUBGKKRECSDACKAYKE
WLQTWKEHYEKQKIKYENDKDSYTNDPDTKQSPQAYQYLNKKLEKICPGGNTSANCEY
KCMKYPBSQNNNNMPABLDDPPSDYKOTCGTYGSASSNFSYNSEDGEBGPPPRAP
RQSLAKSANNSONPSPAPPGGGPPDAGGARAETGPSPQQPPRAPRAP
RQSLAKSANNSONPSPRAPPGGGPPDAGGARAETGPSPQQPPRAPPAGHGGYARIL
PPIARVDQDEEEDBDEBDDEBESGSEEGGGDVDDSDSSEDENDBEDDSHHVDGGH
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DKYQGELDKLNGNSNGNNNCCKEIKGHTSASEFLKELKHCKDGQNSEDDTDKSEEDKK
NNKIDFNKPLETFNPSTYCETCPSNKVNCNGSGRGTRGKDPCTPHNEKGKSWESVFNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EKTDICKLKNFNDKIDLNQYTTFKVFLEYWLQDFIEGYYILKKRKIIEQCKENGGETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NENSKNDCACVKGWVAQKTTEWNQIKDHYNKKEYGNGYDMSHKVKNYFEKNENELRKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               660 CAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATG 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 CTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAAT 839
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HomO.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600 GCAACAACACTGTTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQ741677 300 bp DNA
Sequence 27611 from Patent WO02068579.
CQ741677
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  233823 ATATTGT 233829
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CQ741677
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/organism="Homo sapiens"

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1 (bases 1 to 26188)

State (bases 1 to 26188)

Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anguiano,D., Anguiano,D., Anguianiake,D., Barber,M., Baca,E., Baden,H., Bandaraniake,D., Barber,M., Barnstead,M., Benahmed,F., Baldwin,D., Bandaraniake,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blart,J., Blankenburg,K., Blyth,P., Brown,M., Benahmed,F., Cardenas,V., Carter,F., Cardenas,V., Carter,F., Cardenas,D., Chen,G., Chen,R., Chen,Y., Chen,M., Davia,M., Davia,C., Davila,M., Davis,C., Davy-Carroll,L., De Anda,C., Deferich,D., Delgdo,O., Denson,S., Deramo,C., Coyle,M., Cree,A., D'Souza,L., Delgdo,O., Denson,S., Deramo,C., Durn,A., Durbin,K., Divya,K., Garea,M., Edgen,A., Escotto,M., Eugen,C., Evans,C.A., Falls,T., Fan,G., Farser,C.M., Gabis,A., Garria,R., Garria,A., Garria,M., Hanland,M., Hanla,D., Hanland,Lon,C., Hanland,Lon,C., Hanland,Lon,C., Hanland,L., Havelak,P., Hawes,A., Henderson,N., Hernandez,J., Howells,S., Hulyk,S., Hulyk,S., Kung,L., Kowis, L., Liu,J., Liu,J., Liu,Y., Longare,S., Lopsza,D., Liu,J., Jang,H., Johnson,B., Johnson,R., Johnson,R., Mangum,R., Mangum,R., Mathely,B., Mathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACLZB139 261587 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-104014, WORKING DRAFT SEQUENCE, 7
unordered pieces.
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                                                                                                                                                                                                                                                                672
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 gcagagriggaacaggaaarcccagcarggaacaggaagcarccagcarggaacaggaag 181
                                                                                                                                                                                                                                                                                                                                  61
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        733 CCATACTGTATCAGGGGGGCACAATACCGTATCCGGGAGCAACAATACTGTATCCGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                 673 TATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTGTCTGGAAGCTT
                                                                                                                                                                                                                                                                    TGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGGACAAAGCA
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                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                  ;
                                                                                                                                Length 300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATCCAGCATGGAACAGGGAGCATCCAGAGTGGAACAG 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC126139
AC126139.7 GI:30520607
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                       DB 6;
                                                                                                                                   Ouery Match 6.4%; Score 62.8; DB 6; Best Local Similarity 55.5%; Pred. No. 8.7e-06; Matches 121; Conservative 0; Mismatches 97
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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SOURCE
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AUTHORS
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exon gene

FEATURES

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gene

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Submitted (24-FEB-1999) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK
On Oct 3, 2002 this sequence version replaced gi:5731897.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Similar to Plasmodium falciparum variant-specific surface protein var-2 SWALL:Q26033 (EMBL:L40609) (2664 aa) facta socres: E(): 7.8e-149, 43.1% id in 2872 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /trānslation="MVRTGGSGGGGVDKDGIDHQSAKHLLDSIGKKVHDQVKNGADGT
GASGDAKNYIDDLKGDLQKAPNINPKLIGTDDPCKLVEDYYNNHVNGDGKGERYPCTE
LSGKKFQNPPSDTLGGQCTNSKMRSGCEGACAPYRRLHLCHHNLESIETTSKTASDTL
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TCEVKSGNNYFRATCGDEKNPSLTSKQCRCDKDKAGKPIKGSGNVNIVPTYFDYVPQY
LRWPEEWAEDFCKLRKHKLKDAIKKCRGKNGEEKYCDLNRYDCKNTASGKHVFFEDFD
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KRYYELKGYTKYKVYNNFLEKLMDDOVCTKNDIN INGGANIDFKYHGSARKGDGNNK
TFYRIKYCEA,CFWGGSBKVEGGWKAKEBNCSQTKDYDPDKTTIEILTGDTRKSDNVO
KYKKFCNGNGGNGEKSATPNATSREKGKKGDQMEKWICYYDENKEKKYGSDAINFCVL
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CGCPEKWVKQKKEKEWEA I XDHFGKQKD I I EQTGCDAGVTLAAVLKLEFLNEDTBEKS
EKGLDAEEAKE I KHLRQMLEQAGVRD LAAVGGPCTEGGVAEQNT I MDKFLDEELKEAE
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YYIAHSETRINIETQDDLRDAFIRTAAAETFLEWQYKI KNGADAKQLDNGTIPEBET
RSWYFTYGDYRDICLNTDI SKTVNDVAKAKDKIGKFFSKDGSKSPGGTLTPQDWWQTY
GKDI WKGMICALITHOYTWIEKKTKIKNDYSYDKVNOSQNGNPSLEDFAKKPQFLRWNI
BWGEBFCAERGKLEQNIGKSCNGINPIQYCSDNRHPCNKACDBYKNYVETKQKEFRGQ
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NQGSICVPPRRRKLYVTPLTKWAEBTTKGSKSQBSGKAEGTSESSGSBASSPGGTSSS
GEKSPQGLSTPASTSSPSNSRDDDLLKAFVESAAVETFFLWHKYKMDKQKELDEKKKQ
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PFGIYAHKYSEKCNCLGAKFVPTNVPPAPPPQPPPPAI PAPATTPGVNPCEI VNTLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDSGNTNGSNNNNI VI EASGDKQDEMKKI QKA I DEHI NSLKQAAS V DNPQRPGQQQON
SSLTRETLWKEHAPSI WEGMI CALIY KENDEKKI VKDNEVY EKFFGTTPGTTSGKYKE
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KKKTKSTIDLLRVINIPKSDYDIPTKLSPNRYIPYTSGKYRGKRYIYLEGDSGTDSGY
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VPNDYSSGDIPFNTQHNTLYFDKPDEKPFITSIHDRNLYTGEEYNYDMSTNSGNNDLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="erythrocyte membrane protein 1 (PfEMP1)"
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/bx zref="er:12499127"
/db zref="er:12499127"
/db zref="GA:081220"
/db_xref="UniProt/TrEMBL:081220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Similar to Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                           organism="Plasmodium falciparum 3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(35153, .41725,42757, .44124)
/gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oin(35153. .41725,42757. .44124)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic_DNA"
/isolate="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="rep20 Repeats"
                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="synonym:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome="4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="MAL4P1"
10384. .32958
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        Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                            source
TITLE
JOURNAL
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NGKNNLYSGQNNVYSGIDPTSDNRGLTSGKHDSYSGIDLINDTLSGNQHIDIYDEVLK
KEKELEGTRHVKHTTINFRKPARDDDDLHNQLELHTWLDGHRNMCKELLD
KLKEEWERETHSGWHTHSDSNKTIATDVSIQIDMDNPKPINQFTNMDINVDTPTMDNM
EDDIYYDVNDHDTSTVDSNTMDVPSKVQIEMDVNTKLVKEKYPIADVWDI"
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LYKKATKPGVTTSNNPKDEKDVVDFLKQLLPRKSKNTPGVTAMTPNTLYSSAAGYIHQ
ELGKTVGCNTQKEFCDNKKGKYAFKHPPKEYEBACICDTRQKAQKPIEKKNDCNGIKT
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HVWKPKALBAIJAKAIRGTADIAAAABAAGKARGMEPVIKALKHEGVENFFGICU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISSTGNYTKVTEFVNTIYSKYNGTCNLMRSSINPTACYTIETELSIKTGGAGTGDHPP
LYAIRQMIKGLAEEATEAAKAAEAAKNAKLTAAIKEKQTALIEAGFNSSITSINASII
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RAVFKKINDNLKEKEISDYDNDPNYYKLREDWWTANRDQVWRAITCYIPYYVNYFKKT
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RAMKYSFADI GDI I RGKDMWVQNTDATKLQAYLAKI FDKI KDNHKDI KGKLQYNGDTD
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NNNGGKLVRVKRLAEMMQRRARKQLEKRGGE I NLKADASQGKY I RGGKEKKLNGQI CN
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surface protein var-3 SWALL:Q26032 (EMBL:L40609) (3006 aa)
fasta scores: E(): 6.2e-103, 43.31% id in 3551 aa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDTSYSNDSRNGNNGGPCTGKNDKRFKIGTEWSYGEHEKKRTHPEVYMPPRREHMCIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /noce="1 probable transmembrane helix predicted by TMRHWN2.0 at aa 328-350 Similar to Plasmodium falciparum rifin pfb0030C SWALL:096112 [EMBLAB001367] (370 aa) fasta scores: E(): 3.4e-65, 53.6% id in 375 aa"
                                                                                                                                                                                                                                                                                           could be alternate exon II
                                                                                                                                                                                                                                                                                                                                                                complement (join (48479. .49537,49768. .49821))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join (48479. .49537,49768. .49821))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (join (52002. .53297, 54200. .63307))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AILIIVLIMVIIYLILRYRRKKKMKKKLQYIKLLKE"
complement (join(52002. .53297,54200. .63307))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAD49095.1"
/db_xref="G1:23498128"
/db_xref="UniProt/TrEMBL:Q81219"
                                                                                                                                                                                                                                                                                                                                 upstream VAR gene PFD0005w'
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="synonym: PFD0015c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="synonym: PFD0020c"
                                                                                                                                                                                                                                                                                               /note="VAR exon II,
                                                                                                                                               45458. .46601
/gene="PFD0010w"
                                                                                                                                                                                                                       45458. .46601
/gene="PFD0010w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="RIFIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="VAR"
                                                                                                                                                                                                                                                                                                                                                                                                     gene="RIF"
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gene

CDS

I DKNKGNEEYENYKDKEAHDYLKDKCFPGTCDYMEKVKNNSEYWDKPNKTYTNSDLEK

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Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barron, A., Brooks, K., Buckee, C.O., Burrows, C., Cherevach, I., Chillingworth, C., Christodoulou, Z., Clark, B., Clark, R., Corton, C., Cronin, A., Davies, R., Davies, P., Dear, P., Dearden, F., Doggett, J., Feltwell, T., Goble, A., Goodhaad, I., Gwilliam, R., Hamlin, N., Hance, E., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Horrocks, P., Humphray, S., Jaqels, K., James, K.D., Johnson, D., Kerhornou, A., Knights, A., Konfortov, B., Kyes, S., Larke, N., Lawson, D., Lennard, N., Line, A., Maddison, M., Mclean, J., Mooney, P., Moule, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M.A., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, S., Stevens, K., Taylor, K., Trivey, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J.E., Craig, A., Newbold, C. and Barrell, B.G.
                                                                                                                                                                                                                                                                              /translation="WYIFAYPDDPRYRKDKRGSGIVKFRYRTLEBEYRTQEBEYRTQE
BEYRTQEBEYRTQEKBYRTQEEBYRTQEBEYRTQEKKBYRTQEK
YKTREDEYGTLEBDSEESYETLEDEYGILEDEYRTLEKDSEEBYGSPENEYKIRERY
GTXEEDSEDSEDSEKEYGTLEEDSEBDSEDSEDSEDSELKKEGFIEHRGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INV 29-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 AAGAATATCGTACCCAAGAGGAATATCGTACCCAAGAGGAAGAATATCGTACCCAAG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152 Aggadagatatochacceangagadagatatoggacceangagadagatatograce 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       725 GGAAGCTTCCATACTGTATCAGGGAGCACAATACCGTATCCGGGAGCAACAATACTGTA 784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 aagaggaagaatattggacccgagaggaagaagtataggacccgagagaagaatatagga 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 347582)
Hamlin,N., Pain,A., Berriman,B., Hall,N., Bowman,S., Churcher,C.,
Harris,B., Harris,D., Lawson,D., Quail,M. and Barrell,B.
                                                                                           /gene="rpoC2"
/note="grass-specific insert; similar to Oryza sativa
sequence deposited with GenBank Accession Number X15901"
                                                                                                                                                                                                           product="DNA-directed RNA polymerase beta' subunit 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         665 ACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAATGTGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          605 AACACTGTTGTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTATCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13 Nature 419 (6906), 527-531 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 cccaagagaaararccraccaagagaaaagaaagacccga 318
                                                                                                                                                                                                                                                                                                                                                                                                                            Length 646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      831
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.5%; Score 63.8; DB 8; Length 6 Best Local Similarity 55.1%; Pred. No. 5.4e-06; Matches 125; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGA
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db_xref="taxon:158113"
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Plasmodium falciparum MAL4P1.
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/db_xref="GI:16551243"
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Plasmodium falciparum 3D7
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AL034557.8 GI:23498126
                                                                                                                                                                      start=1
                           <1. . . > 646
/gene="rpoC2"
                                                                        .>646
                                                                                                                                                                                     /trans]
                                                                                                                                                                 codon
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ACCESSION
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REFERENCE
AUTHORS
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                             gene
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19473 ACAGGAAGCATCCAGAGTGGAACAGGAAACGTCCACCATGGAACAGGAAGCATCCAGAGT 19532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19533 GGAACAGGAAGCATGCAGAGTGGAACAGGAAATGTCCAGCATGGAACAGGAAGCATCCAG 19592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF372178 646 bp DNA linear PLN 18-JUN-2002 Leptocoryphium lanatum DNA-directed RNA polymerase beta' subunit 2 (rpoC2) gene, partial cds; chloroplast gene for chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Paniceae, Leptocoryphium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Duvall, M.R., Noll, J.D. and Minn, A.H.
Direct Submission
Submitted (18-APR-2001) Biological Sciences, Northern Illinois
University, Montgomery Hall, DeKalb, IL 60115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              659 TCAGGGACAAAGCATATTGTTACTGATAACAATAATGTTGTATCCGGGAACGACAATAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  599 AGCAACAACACTGTTAACTGGAAGTGACAATACTGTAGTTGGTAGCAACCATGTCGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dbSTS:STS23199
Identified using the e-PCR software (G. Schuler)"
                             (G. Schuler) "
                                                                                                                                                                                                                                                                    Schuler) "
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                                                                                                                                                  Schuler)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 169802;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        779 ACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAG
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                           Identified using the e-PCR software 39203. .39300
                                                                                                                                                                                                                     RHdb:RH71306
dbsTS:STSE1071
Identified using the e-PCR software
131895. .132128
                                                                                                                                                Identified using the e-PCR software
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.9%; Score 67.2; DB 9; 55.6%; Pred. No. 1.8e-06; iive 0; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organelle="plastid:chloroplast"
/wol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 646)
Duvall, M.R., Noll, J.D. and Minn, A.H.
Phylogenetics of Paniceae (Poaceae)
Am. J. Bot. 88 (11), 1988-1992 (2001)
2 (bases 1 to 646)
                                                                                                                                                                   39281. 39447
/note="matching EMBL:X99549
                                                    19203. .39300
'note="matching EMBL:G14654
                                                                                                                                                                                                                                                                                                                 note="matching EMBL:X00253
                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="matching EMBL:R05773
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Leptocoryphium lanatum
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AF372178.1 GI:16551242
                                                                                                                              dbSTS:STS21065
                                                                                                                                                                                                                                                                                                                                                                     dbSTS:STS3713
                                                                                                                                                                                                                                                                                                                                            RHdb: RH18069
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                                                                                                        RHdb:RH797
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DEFINITION
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TITLE
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VERSION
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AF372178
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SOURCE
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CNS01DT2 169802 bp DNA · linear PRI 19-NOV-2001 Human chromosome 14 DNA sequence BAC R-417P24 of library RPCI-11 from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mamalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Bass 1 to 16.0.)

Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wincker,P., Brottier,P., Cattolico,L., Barbe,V., Pelletier,E., Artiguenave,F., Gyapay,G., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (19-NOV-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 ENRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr
On Nov 20, 2001 this sequence version replaced gi:14715169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The following BAC sequence is oriented from the T7 to the SP6 end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identified using the e-PCR software (G. Schuler)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dentified using the e-PCR software (G. Schuler)"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Genoscope / Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.genoscope.cns.fr/
Contact: SegRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="matching EMBL:G33053
RHdb:RH67749
dbSTS:STS47676
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/note="matching EMBL:G33053
RHdb:RH67749
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/note="matching EMBL:G14654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic_DNR/db_xref="taxon:9606"
/chromosome="14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="R-417P24"
/clone_lib="RPCI-11"
11427._.11641
                                                                                    AL122127.6 GI:17026193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Overall quality chart :
Range : bases
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                                                                                                                                                                                                                                                                                                              (bases 1 to 169802)
                                                                                                                      Homo sapiens (human)
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159
4325
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69316. .69421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="matching EMBL: AA160692
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RHdb:RH68981
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/note="matching EMBL:M55420
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                                                                                                                                                                                                             1. .176237
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/clone_lib="RPCI-11"
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Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Kucosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, O., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawanata, M., Yoshimura, A., Mura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RikEnsi, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., RikEnsi, Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y., Shinagawa, A., Shiraki, T., Yoshino, mapping, and annotation of over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lough, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, Hayanco, K., Hiraoka, T., Hayashizaki, Y., Hayatsu, N., Hiramco, K., Hiraoka, T., Horta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kadawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kojima, Y., Miura, J., Miyazaki, M., Masuda, H., Matsubara, K., Mateuyama, T., Miyazaki, M., Masuda, H., Matsubara, K., Mateuyama, T., Miyazaki, M., Murakami, K., Mata, M., Ohneda, E., Ohno, M., Ohtsuki, K., Oha, M., Ooka, M., Ooka, M., Osato, N., Caro, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Shinagawa, A., Shiraki, T., Saitoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tomaru, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami, Takeda, Y., Tomaru, A., Yamada, A., Yanada, M., Yasunishi, A., Yazaki, J., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
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FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Rujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,
Kodama, T., Kusumegi, T., Lu, M., Mana, J.,
Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,
Sugiyama, A., Matubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Exploration Research Group in Riken: Adachi, J., Alzawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,
Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
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Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
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Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.
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UKL. http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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Direct Submission

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Agrobiological Sciences, Department of Molecular Genetics, Head of

Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki

25-602, Japan (E-mail:skikuchi@mias.affrc.go.jp,

Tel:81-29-838-7007, Fax:81-29-838-7007, Tax:81-29-838-7007, Tax:81-2
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CNSOBCBF
Human chromosome 14 DNA sequence BAC R-731F5 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
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1 (bases 1 to 17621)

1 (bases 1 to 17621)

Entrier, P., Petit, J.L., Vico, V., Dasilva, C., Robert, C., Wincker, P., Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F., Gyapay, G., Saurin, W. and Weissenbach, J. Sequencing of the human chromosome 14

Unpublished
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On Sep 24, 2002 this sequence version replaced gi:23306222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 CGGGTAATTCATTGGTTTGGGGAGGTACCAAAAAGTTTGCAGATACGGCTCAAGAGCCTCA 410
                                                                                                                                                                                                                                                                                                                                           291 TTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTATTTGGATCTCT 350
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    2958
/organism="Oryza .sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                         3,
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                                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                                                                    7.6%; Score 74.8; DB 8; Local Similarity 68.4%; Pred. No. 7.5e-09; es 119; Conservative 0; Mismatches 52
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Contact: SeqRef@genoscope.cns.fr
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Location/Qualifiers
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Homo sapiens
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Matches 119; Conservative
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Yamamoco, M.

FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,

Rujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Kodama, T., Kurikawa, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Mizuno, K., Narikawa, R., Nikura, J., Oka, M., Ryu, R., Sugano, S.,

Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,

Sugiyama, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K.,

Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,

Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,

Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, M., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,

Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Tayahashi, F.,

Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,

Yasunishi, A., and Hayashizaki, Y.
                                                                                                                          URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2958 bp mRNA linear PLN 24-JUL-2003
Oryza Bativa (japonica cultivar-group) cDNA clone:J033121E13, full
AK103166
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rel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AK103166.1 GI:32988375
FIZ. CAP trapper.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 CGGGTAATTCATTGGTTGGGGAGGTACCAAAAAGTTTGCAGATACGGCTCAAGAGCCTCA 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 TCACCGCCGGCGTTCGCCGGTATGGCGTTCACTAACATGCCGTTGTATGTGA 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Oryza sativa (japonica cultivar-group)"
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68.4%; Pred. No. 7.1e-09;
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/cultivar="Nipponbare"
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/clone="002-108-B08"
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Matches 119; Conservative
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                                        COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobaysahi, M., Xie, Q., Lu, M., Narikawa, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Mitura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., Rikkni, Kawai, J., Carninci, P., Adachi, J., Alzawa, K., Rikkni, Kawai, J., Adachi, J., Alzawa, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saitoh, R., Sahira, K., Shinagawa, A., Shiraki, T., Shini, Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Colley, M., Adachi, Y., Shinagawa, A., Shiraki, T., Colley, Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Colley, M., Adalo, S., Shiraki, T., Colley, Sato, S., Shiraki, T., Colley, Sato, S., Shiraki, T., Colley, Sato, S., Shiraki, T., Shini, S., Shiraki, T., Colley, S., Shinagawa, A., Shiraki, T., Colley, S., Shini, S., Shiraki, T., Shini, S., Sh
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                                                                                                   273194 TGGTGGATGATGAACAACAATATGGTGGATGATAACAACAACAATATGGTGGATAATCACAATA 273135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (japonica cultivar-group) cDNA clone:002-108-B08, full AK064359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKO64359.1 GI:32974377
FLI_CDNA; oligo-capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression, 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
                                             CCGTATCCGGGAGCAACAATACTGTATCCGGGAGCAACCATATCGTATCTGGGAGCAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            japonica rice
Science 301 (5631), 376-379 (2003)
                                                                                                                                                                                                                                                                                                      273134 CTATGCGTAGCGAAGATGAA 273115
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JOURNAL
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AUTHORS
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2732554 TGGATGATAACAACAATATGGTGGATGATAACAACAATATGGTGGTGGATGATAACAACAATA 273195
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KMSRYTDVTKFGAAIAEKHVLNCAMSARGGSVNDSTCNAFEIKLGLFEAETGKPNGPP
YQAIPQKINELAEEATQAAAEAAKKASESATAAFETAEKEAIEASMQLYTTIAYSI
LAILIIVINVIIVLIRYRKKKKKKLOYIKLEE"
complement (join (18586. 19821,19980. 22721))
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QNRFDENAEAYCNSDKRAGGWGVRYGPANSCDLEHRFYTNINNGYLPARNPCHNRN
QNRFDENAEAYCNSCRRGENNSNAGACAPFRRQNLCDKNLEYLINENTKTYHDLLG
NVLVTAKYEGDYIVNNHPNRGSSEVCIALARSFADIGDIVRGKDMFKSNDNVENGLRE
VFKKIYEGFLDKGARRHYKEVKNGNGYIIKLREDWAYANRDQWKAAMTCVAPRENNYFRKT
EADGIGISSLILPYSKCGRDTDPPVVDYIPQLRWMSEWSFFCNVLNKEIDENNNQ
KDCEMSRRCNNDTGBEKCKKCKEQCOIFKELVSKWNREDKGSMKYKELYIKASTNIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENYDNIEGSNRPNAFEIPPEKFKKACKCKIPNPLEKCPNEENKUVCTRFDKVSSCTSL
PERNDIE BRANNSGVENENDROUVLPPRRRNLLCTUNESKOOY KRANDENBELLAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DRNLYTGEEI SYNINMSTNTNNDI PKYVSNNVYSGIDLINDTLSGNKHIDIYDEVLKR
KENELFGTNHVKQTSIHSVAKNTYSDDAITNKINLFHKMLYRHRDMCEKWENHHERLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLKEKWENDNDGGNVPSDNHVLNTDVSI EI DMDNPKPI NQFSNMDINVDTPTMDNMED
DI YYDVNDNDDDDNDQPSVYDI PMDHNKVDVDVPKKVHI EMKI LNNTSNGSLEQQFPI S
                                                                                                                                                         YAPATYDDDPQMKEVMQQFEDRTSQRFHEYDERMKTTRQKCKDKCDKEIQKIILKDKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YKLIDEEWNQLKDDFISQYLPNTEPNNNYRSGNSPINTNNTTTSHDNMGEKPFIMSIH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273374 ATAACAACAATATGGTGGATGATAACAACAATATGGTGGATGATAGCAACAATATGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         273314 ATGATAACAACAATATGGTGGATGATAACAACAATATGGTGGTGGTGATAACAACAATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 TATCCGGGAACGACAATAATGTGTCTGGAAGCTTCCATACTGTATCAGGGGAGCACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 579 ATAACAACCATGTGTCTGGGAGCAACAACACTGTTGTAACTGGAAGTGACAATACTGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           639 TIGGIAGCAACCAIGICGIAICAGGGACAAAGCAIATIGIIACIGAIAACAAIAAIGIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Does not produce Pfam hit to PFEMP domain [pfam:PF03011], found in Pfempl protein family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /locus_tag="PFF0020c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(26557. .26610,26766. .27830)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="RIF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="VAR-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAL6P1.314'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein"
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                                                                                                                                                                                                                                                                                                                                                                                                              gene
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VMHSPLGDVILAAMBRAKKI KELYTKONGLNDLKOKETVORAMKYSFADLGDI I RGRU
VMRAMKCA I KEAT I DINCNGI PI EDY I PORLIKWYTEWAEWAWYCKOGSGYKKLODACTGC
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PGAGES PARSDADSRGPATVOKAGEVEDDBEVDSEBEEDEVBEEPPREEVCEWYDTLL
DESNGGKNGI NGCNPKDQVQPY PGWDCKLSTPKDKEHGS CMPPRR I KLCVSGLTQTNN
I INREDI RTHIFT TAAA I ETY YSTAT LEKENGTKS BEPERGKKI TYTTFGDYR
DI FPGTD I STHNH I PEWSSKYJ I IL I KERNGTKSBE PERGKKYTTD
KVQPEYAVDADVKKSTHAYOYL SKYLKKI CONGTTTDKCONTYLDEDWKKEHGPE I WEG
MLCALTNGLTDDEKKNEI KTKYSYDELANAKKCERECKYVEGPI KOWTTTDKCONGTTTD
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ILKNYKEQURTDKYNTY DLAS DWWARREI I REMITKOVDBKUFFPQVVMKAAKEBGIR
ILKNYKEQURTDKYNTY DLAS DWWARREI I KKANYTONGKYT RYTYTEN
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VQDDIYYDVNDHDASTVDSNAVNVPSKVQIEMDVNTKLVKEKYPIADVWDI"
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CRDSNDGNNCRKCQQNCQEYTKLVNQCKKQF I LQDNQYKEI YKKI SNNSDGKAYVGTH
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YYKSFYKKFAKSDYKKVHDFLTLLNNGRYCKEGVDGKDAI DFNKTDDKDAFDRSEYCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCPACVVECDGGKCEEKKNSDGTCIEAQIYTVVRDETPTFIKVLFSGDHQKDITKKLS
SFCKNPESENNRDYQTWQCYYKSSDYNNCEMKGSLYKVEGDPNIIVSHECFHLMVQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIDTIKWETKLKKCINNTNVTNCYNKCNKNCECFENWVEQKKKEWENVNDVYKDQÑQS
LGIYYEKLENLFKSNFFQVMKALEGDEKGKWYQFKDDLKKKFEPSEKNTRTTDSQDAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLILDHLKDNATTCKDNNSLEEDENCPKTKINPCIKRTRIPTRGASNNLVSVKHIAEL
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AGKOTGRFDIGTPWKTGTNVKMTEDQAYMPPRREHMCTSNLEYLETDQGPLKNSDGKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGLDLLKNHSCNYELTQYIGWNTMVKQYMDGFDIKFQKVKNASTNSSISENSAQEYIK
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EEDTSHVQPPPLPPKPSTPEVEPLPSDEPFDPTILQTTIPFGVALALGSIAFLFLKKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLSPVDLFSVINIPKGDYNIPTLKSSNRYIPYASDRYKGKTYIYMEGDSSGDEKYAFM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDTTD1TSSESEYEELD1ND1YVPRAPKYKTL1EVVLEPSKSNGNTLGDD1PHTNKFT
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LYSGEEYSYNVMWVNSMDDI PINRDNNVYSGI DLINDTLSGNKHIDI YDEVLKRKENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFGTNHTKKNTSTNSVAKNTNSDPILNQINLFHTWLDRHRDMCEKLKNDNERLAKLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KNNYPHTNI CTVLARSFADIGDI VRGKDLFLGHQQRKRKLEENLKQMFENI KKNNDKL
DKISIEQVREYWWNANRDQVWEAITCHAAHSDEYFRKSTDGVTLYFDGRCGRELSSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASSSILGETASTDKPCTFEYNKLLGARGKRHPCGNRQTVRFSDEYGGQCTFNRIKDSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYLDYVPQFLRWFDEWSEEFCRKRNITLKSAKEECQNDSKKLYCSLNGYNCTRLIPNK
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273315

gene

CDS

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Eukaryota, Alveolata, Apicomplexa; Haemosporida; Plasmodium.

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1 (bases 1 to 349418)

RS Hall,N., Pain,A., Berriman,M., Churcher,C., Harris,B., Harris,D.,

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Chillingworth,T., Christodoulou,Z., Clark,L., Clark,R., Corton,C.,

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Rabbinowitsch,E., Rajandream,M.A., Rutter,S., Rutherford,K.M.,

Squares,S., Stevens,K., Taylor,K., Tivey,A., Unwin,L.,

Mitchead,S., Woodward,J., Sulston,J.B., Craig,A., Newbold,C. and

Barrell,B.G.

By Nature 419 (6906), 527-531 (2002)
                                       349418 bp DNA linear INV 30-MAR-2004 Plasmodium falciparum chromosome 6, complete sequence; segment 1/5. CR382398 AL644505 FT. GR382398.1 GI:46362238 FTG.
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Unpublished
(Uppublished
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(Bases 1 to 349418)
(Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berriman, M., Pain, A., Hall, N., Atkin, R., Chillingworth, C.,
nogaett, J., Ormond, D., Sanders, M., Hayes, R., Hall, S., Quail, M. and
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Submitted (20-SB2-2002) P.falciparum Genome Sequencing Consortium,
The Welcome Trust Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 18A, UK
Hinxton, Cambridge CB10 18A, UK
4 (Dases I to 349418)
Cherevach, I., Davis, P., Goodhead, I., Stevens, K., Mungall, K.,
Berry, A.E., Berriman, M., RA Pain, A., Hall, N., Atkin, R.,
Hall, S., Quail, M. and Barrell, B.G.
Direct Submission
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For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
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/isolate="3D7"
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/locus_tag="PFF0005c"
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                                                                                                                                                                                                                       Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .349418
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                              RESULT 6
CR382398/c
                                                                                                          DEFINITION
ACCESSION
VERSION
KEYWORDS
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EEYGSGGCSVKSKTWNERKLCTKRGTCRAEGFDYGSCYPNRPRPSFIGRFFHVCYCSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 GCAACGTCGTGGTCGTGCCACCACGACGACCTCCACGCGTTGAGGGGCCTCGCTGAGAAC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 AGCTGGGAAGGTGTGGGATGCGAAACAGCAGCGGCCGCGTCGTGGGCGTTGCGGCTCCCC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       281 AAGCGCGCCCTTGGAGGGATCATCCCATCGTCGATTGGTGAGCTTGATCACCTTCGCTAT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="contains EST(s): AU056601(S20723), AU056602(S20723)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CT---AAGCGGCAAAGGAGCCGTCCGCCTCCGCGCCGCATGGTCCGGCGCCTCATGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26456 GCCTGGGACGCCTGCGACGCCGC---CGCCCGAGTCACGGCGCTGCGCCTCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26336 GCTGCGGCGGCCCATGCCACCCGGAAGACCTCCTCGCGCTGCGGGCATTTGCGGGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 79.4; DB 8; Length 149371;
Pred. No. 8.9e-10;
0; Mismatches 86; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complainent (20109. .20613)
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complement (join (20109. .20350,20514. .>20613))
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/note="start and end point are not identified"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative phytosulfokine receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGDGEHPQPSRSLVAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
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Best Local Similarity 63.1
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26573 CTCGACCTC 26581
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complement (5704. .6661)
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aaaagqrdrvtrtartartarhgrqprgrarandargaaarerrgelgsapalahaargqs
gaegerarekeserregggdgpreirpldpgggkidfcggi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      non-coding transcript probably inactive due to including stop codon(s) in CDS" complement(5942...6631) //gene="P0585H11.104" //note="contains EST(s): AU101213(E2609),C72987(E2609) contains full-length cDNA(s): AK106062"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(5704. .6661)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(<8221. .8529,8623. .>8754))
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complement(1507, .1932)
/gene="P0585H11.102"
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                                                                                                                                                                                                                                                                                                             'note="predicted by GlimmerM etc."
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/note="free"
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/gene="P0585H11.106"
                                                                                                                                                   complement (<1507...>1932)
/gene="P0585H11.102"
                                                                                             complement (1507. .1932)
/gene="P0585H11.102"
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/gene="P0585H11.105"
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                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="similar to Oryza sativa chromosome 1, P0409B08.8"
                                                                                                                                                                                                                                                                                                                                             Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
Submitted (14-NOV-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                       Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 7, PAC clone:P0585H11
Published Only in Database (2001)
2 (bases 1 to 149371)
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
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/gene="P0585H11.101"
/note="start and end point are not identified"
complement(join(298..591,655..792))
/gene="P0585H11.101"
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/protein_id="BAC20734.1"
/db_xref="G1:23617046"
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/gene="P0585H11.101"
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/clone="P0585H11"
                SOURCE
                                                                                                                                                                REFERENCE
AUTHORS
TITLE
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AUTHORS
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JOURNAL
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Falls Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Falls Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobaysahi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Kobaysahi, M., Kodama, T., Kuronogi, T., Lu, M., Masuda, H., Miura, J., Mikura, J., Matsubara, K. and Murakami, K. Sigano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yokhimura, R., Matsubara, K. and Murakami, K. Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carnind, P., Hayatsu, M., Hiramoto, K., Hayatsu, M., Hiramoto, K., Harahizume, W., Hayashida, K., Hayatsu, M., Hiramagaki, T., Kanagawa, T., Kanadawa, S., Karob, S., Konno, H., Konda, M., Kishikawa-Hirozane, T., Matsuyama, T., Miyazaki, A., Murata, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Sahamura, M., Saho, H., Sakai, C., Sakai, K., Shibata, K., Saitoh, H., Sakai, T., Sato, K., Shibata, K., Saitoh, H., Sakai, T., Tagami, M., Tagami, Takaku-Akahira, S., Tanaka, T., Tagami, M., Taya, T., Tagami, M., Tayaki, K., Tagami, M., Tayaki, T., Tagawa, T., Tagawa, T., Tagami, K., Tagami, M., Tayaki, K., Tayaki, K., Taya, T., Waki, K., Yasunishi, A., Takahashi, Y., Taya, T., Waki, K., Yasunish
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chromosome 7,
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    305-8602, Japan (E-mail:skikuchi@nias.attrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 32K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 GCAACGTCGTGGTCGTGCCACCACCACGACGTCCACGCGTTGAGGGGCCTCGCTGAGAAC 163
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
Yamamoto,M. and Nakahama,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           322 GCCTGGGACGCGTCGCCTGCGACGCCGC---CGCCCGAGTCACGGCGCTGCGCCTCCCC
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Pred. No. 4.4e-10;
0; Mismatches 86; Indels 6:
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Japan (E-mail:skikuchi@nias.affrc.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J033108010"
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Best Local Similarity 63.1%;
Matches 157; Conservative (
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kishimoto, N., Sazaki, T., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group:, Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fulimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Ishiki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mazuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Voshimura, A., Miura, J., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Kagawa, I., Kondo, S., Kanono, H., Miyazaki, A., Csato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y., Collection, mapping, and annotation of over 28,000 cDNA clones from
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ELI CDNA, CAP trapper.

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
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                                                782 GTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAGTCGTAACAGATGGTTAA 838
                                                                                                 301 GTATCTGGGAGCAACCACGTTGTATCTGGAAGCAAAGTCGTGACAGACGCTTAA 357
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/codon_start=1
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                                                                                                                                                             mRNA linear PLN 29-APR-2000 ice recrystallisation inhibition
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Submitted (11-ARR-2000) Sidebottom C.M., Plant Science, Unilever
Research, Colworth House, Sharnbrook, Bedfordshire, MK44 1LQ,
UNITED KINGDOM
cds represents presumed mature peptide generated by cleavage before
the first amino acid.
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Lolium.
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/product="ice recrystallisation inhibition protein"
/note="ORF1"

GTATCCGGGAGCAACCATATCGTATCTGGGAGCAACAAAGTCGTAACAGATGGTTAA
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/function="freezing tolerance"</pre>
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                                                                                                                                                                    157 bp 2577399 Lolium perenne partial mRNA for
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Pred. No. 2.4e-60;
0; Mismatches 58;
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/mol_type="unassigned DNA"
/db_xref="taxon:4522"
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Sequence 2 from Patent WO9937782
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PN 12-0250416-A/1
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PN 1
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AC126053 Mus muscu
AC099698 Mus muscu
AC090126 Mus muscu
CR522870 Desulfota
AC145777 Ciona sav
AC116699 Mathanosa
AC116699 Mathanosa
AC116699 Rattus no
AC139177 Ciona sav
AC119995 Rattus no
AC134239 Rattus no
AC133239 Rattus no
AC133239 Rattus no
AC133239 Rattus no
AC13361 Trichoder
B02599 DNA encodin
X12843 Human sigma
AC103606 Mus muscu
AL672010 Mouse DNA
AL034557 Plasmodiu
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1 (bases 1 to 357)

2 Adaman, C.D., Sidebottom, C.M., Twigg, S. and Worral, D. Freezed foods
Patent: JP 2002504316-A 1 12-FEB-2002;
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/organism="Lolium perenne"
/mol type="genomic DNA"
/db_xref="taxon:4522"
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AC09958
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AC119495
AC133239
AC095765
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AL672010
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JP 2002504316-A/1.
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5.5 243174

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AJ277399 Lolium pe
AX121984 Oryza sat
AR064359 Cryza sat
CR382398 Plasmodiu
AK064359 Oryza sat
AX103166 Oryza sat
AX103166 Oryza sat
AX103167 Pluman chr
AL122127 Human chr
AL122127 Human chr
AL034557 Plasmodiu
CQ741677 Sequence
AC126139 Rattus no
AC08110701 Rattus no
AC0811071 Rattus no
AC0811073 Rattus no
AC081137 Rattus no
AC091137 Rattus no
AC091137 Rattus no
AC091137 Rattus no
AC091137 Rattus no
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                          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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8.1 149371
7.8 349418
7.6 2238
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27.0
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8.1
7.8
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6:
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770.2
67.2
63.8
62.8
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264.2
79.4
79.4
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Minimum DB E Maximum DB E

Database

Searched:

Sequence:

е 6

PAT 18-SEP-2002

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Gaps

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Result No.